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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2003, 12:26:17 ; Search time 77 Seconds
(without alignments)
3115.017 Million cell updates/sec

Title: US-09-899-440-18
Perfect score: 2850
Sequence: 1 MLLRSKPALPPPLLMLLLLG.....LPAFSYSFFVIRNAKVAACI 545

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 201138

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=40 -USER=US09899440_@CGN_1_1_35_@runat_08012003_124404_23198 -NCPU=6
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	53	1.9	24	9	US-09-988-113-7	Sequence 7, Appli
c	3	53	1.9	24	9	US-09-988-113-29	Sequence 29, Appl
c	4	53	1.9	24	10	US-09-759-207-7	Sequence 7, Appli.
c	5	53	1.9	24	10	US-09-776-874A-2	Sequence 2, Appli
c	6	53	1.9	24	10	US-09-776-874A-7	Sequence 7, Appli
c	7	53	1.9	24	10	US-09-776-874A-29	Sequence 29, Appl
c	8	53	1.9	24	10	US-09-944-602-7	Sequence 7, Appli
c	9	53	1.9	24	10	US-09-322-977-7	Sequence 7, Appli
	10	42	1.5	36	10	US-09-504-231A-1888	Sequence 1888, Ap
	11	42	1.5	36	10	US-09-274-553D-1888	Sequence 1888, Ap
	12	41	1.4	40	10	US-09-915-060-21	Sequence 21, Appl
c	13	40	1.4	24	9	US-09-864-321-2	Sequence 2, Appli
c	14	40	1.4	33	9	US-09-337-946A-12	Sequence 12, Appl
c	15	40	1.4	36	10	US-09-504-231A-2742	Sequence 2742, Ap
c	16	40	1.4	36	10	US-09-274-553D-2742	Sequence 2742, Ap
	17	40	1.4	38	9	US-09-864-785-1253	Sequence 1253, Ap
	18	39	1.4	31	10	US-09-801-274-849	Sequence 849, App
c	19	39	1.4	31	10	US-09-801-274-875	Sequence 875, App
c	20	38	1.3	22	10	US-09-930-218-14	Sequence 14, Appl
	21	38	1.3	23	9	US-09-988-113-6	Sequence 6, Appli
	22	38	1.3	23	9	US-09-988-113-25	Sequence 25, Appl
	23	38	1.3	23	10	US-09-759-207-6	Sequence 6, Appli
	24	38	1.3	23	10	US-09-776-874A-6	Sequence 6, Appli
	25	38	1.3	23	10	US-09-776-874A-25	Sequence 25, Appl
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	28	38	1.3	27	9	US-09-956-342-4	Sequence 4, Appli
	29	38	1.3	38	9	US-09-864-785-1236	Sequence 1236, Ap
	30	38	1.3	38	9	US-09-864-785-1335	Sequence 1335, Ap
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c	32	37	1.3	25	10	US-09-866-108-11653	Sequence 11653, A
	33	37	1.3	35	9	US-09-866-248A-26	Sequence 26, Appl
	34	37	1.3	36	10	US-09-504-231A-1738	Sequence 1738, Ap
c	35	37	1.3	36	10	US-09-504-231A-1879	Sequence 1879, Ap
	36	37	1.3	36	10	US-09-274-553D-1738	Sequence 1738, Ap
c	37	37	1.3	36	10	US-09-274-553D-1879	Sequence 1879, Ap
	38	37	1.3	37	10	US-09-504-231A-3188	Sequence 3188, Ap
c	39	37	1.3	37	10	US-09-924-439-10	Sequence 10, Appl
	40	37	1.3	38	9	US-09-864-785-945	Sequence 945, App
	41	37	1.3	38	9	US-09-864-785-1256	Sequence 1256, Ap
	42	37	1.3	38	9	US-09-864-785-1257	Sequence 1257, Ap
	43	37	1.3	38	10	US-09-752-110A-17	Sequence 17, Appl
c	44	37	1.3	39	10	US-09-858-075A-9	Sequence 9, Appli
	45	37	1.3	40	10	US-09-752-110A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-988-113-2/c
; Sequence 2, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVI
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-2

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	9	Gaps:	0

US-09-899-440-18 (1-545) x US-09-988-113-2 (1-24)

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Qy     293 AspSerValThrTrpHisHisTyr 300
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Db      24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 2
US-09-988-113-7/c
; Sequence 7, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-7

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	9	Gaps:	0

US-09-899-440-18 (1-545) x US-09-988-113-7 (1-24)

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Db      24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 3
US-09-988-113-29/c
; Sequence 29, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVI
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-29

Alignment Scores:

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Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	9	Gaps:	0

US-09-899-440-18 (1-545) x US-09-988-113-29 (1-24)

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Db      24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 4
US-09-759-207-7/c
; Sequence 7, Application US/09759207
; Patent No. US20020004585A1
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker et al.
; TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES
; AND THEIR USE IN RESEARCH AND MEDICAL
; APPLICATIONS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: G. E. Ehrlich (1995) Ltd.
; c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; an ASCI file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,207
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/922,180
; FILING DATE: September 2, 1997
; APPLICATION NUMBER: 09/071,739

; FILING DATE: May 1, 1998
; APPLICATION NUMBER: 09/322,977
; FILING DATE: June 1, 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Sol Sheinbein
; REGISTRATION NUMBER: 25,457
; REFERENCE/DOCKET NUMBER: 00/21505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-6127676
; TELEFAX: 972-3-6127575
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-759-207-7

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-759-207-7 (1-24)

Qy 293 AspSerValThrTrpHisHisTyr 300
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Db 24 GATTCAGTTACATGGCATCACTAC 1

RESULT 5
US-09-776-874A-2/c
; Sequence 2, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22603
; CURRENT APPLICATION NUMBER: US/09/776,874A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-776-874A-2

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-776-874A-2 (1-24)

Qy 293 AspSerValThrTrpHisHisTyr 300
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Db 24 GATTCAGTTACATGGCATCACTAC 1

RESULT 6
US-09-776-874A-7/c
; Sequence 7, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVI
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22603
; CURRENT APPLICATION NUMBER: US/09/776,874A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-776-874A-7

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-776-874A-7 (1-24)

Qy 293 AspSerValThrTrpHisHisTyr 300
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Db 24 GATTCAGTTACATGGCATCACTAC 1

RESULT 7
US-09-776-874A-29/c
; Sequence 29, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky , Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVI
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22603
; CURRENT APPLICATION NUMBER: US/09/776,874A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide
US-09-776-874A-29

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-776-874A-29 (1-24)

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Qy    293 AspSerValThrTrpHisHisTyr 300
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Db     24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 8
US-09-944-602-7/c
; Sequence 7, Application US/09944602
; Patent No. US20020102619A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Friedman , Yael
; APPLICANT: Perets, Tuvia
; TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES AND THEIR USE IN RESEARCH AN
; TITLE OF INVENTION: MEDICAL APPLICATIONS
; FILE REFERENCE: 01/22380
; CURRENT APPLICATION NUMBER: US/09/944,602
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 09/759,207
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 09/322,977
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/071,739
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 08/922,180
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-944-602-7

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-944-602-7 (1-24)

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Qy    293 AspSerValThrTrpHisHisTyr 300
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Db     24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 9
US-09-322-977-7/c
; Sequence 7, Application US/09322977
; Patent No. US20020114801A1
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker et al.
; TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES
; TITLE OF INVENTION: AND THEIR USE IN RESEARCH AND MEDICAL
; TITLE OF INVENTION: APPLICATIONS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,977
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/922,180
; FILING DATE: September 2, 1997
; APPLICATION NUMBER: 09/071,739
; FILING DATE: May 1, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 910/21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-322-977-7

Alignment Scores:

Pred. No.:	33	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-322-977-7 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 10
US-09-504-231A-1888
; Sequence 1888, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1888
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-09-504-231A-1888

Alignment Scores:

Pred. No.:	1.21e+03	Length:	36
Score:	42.00	Matches:	7
Percent Similarity:	90.91%	Conservative:	3
Best Local Similarity:	63.64%	Mismatches:	1
Query Match:	1.47%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-504-231A-1888 (1-36)

```
Qy    479 LysTyrLeuLeuArgProLeuGlyProHisGly 489
          :::|||||:::|||||||||||||   :::|||
Db      2 CGGUAUCUGAUGAGGCCGUUAGGCCGAAACGGA 34
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RESULT 11
US-09-274-553D-1888
; Sequence 1888, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1888
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molec
US-09-274-553D-1888

Alignment Scores:

Pred. No.:	1.21e+03	Length:	36
Score:	42.00	Matches:	7
Percent Similarity:	90.91%	Conservative:	3
Best Local Similarity:	63.64%	Mismatches:	1
Query Match:	1.47%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-274-553D-1888 (1-36)

```
Qy    479 LysTyrLeuLeuArgProLeuGlyProHisGly 489
          :::|||||:::|||||||||||||   :::|||
Db      2 CGGUAUCUGAUGAGGCCGUUAGGCCGAAACGGA 34
```

RESULT 12
US-09-915-060-21
; Sequence 21, Application US/09915060
; Patent No. US20020049181A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; TITLE OF INVENTION: No. US2002004918lAlel internal ribosome entry site, vector con
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 2676-4976US
; CURRENT APPLICATION NUMBER: US/09/915,060
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 99200216.2
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E-tag probe
US-09-915-060-21

Alignment Scores:

Pred. No.:	1.88e+03	Length:	40
Score:	41.00	Matches:	7
Percent Similarity:	66.67%	Conservative:	1
Best Local Similarity:	58.33%	Mismatches:	4
Query Match:	1.44%	Indels:	0
DB:	10	Gaps:	0

US-09-899-440-18 (1-545) x US-09-915-060-21 (1-40)

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Qy    344 GlyGluThrSerSerAlaTyrGlyGlyGlyAlaPro 355
          |||   :::   |||   ||||||   |||||||||
Db      5 GGTTCCAGCGGATCCGGATACGGCTCCGGCGCACCT 40
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RESULT 13
US-09-864-321-2/c
; Sequence 2, Application US/09864321
; Publication No. US20020194625A1
; GENERAL INFORMATION:
; APPLICANT: Zcharia, Eyal
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Metzger, Shula
; APPLICANT: Pecker, Iris
; APPLICANT: Ilan, Neta
; APPLICANT: Chajek-Shaul, Tova
; APPLICANT: Goldshmidt, Orit
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING HEPARANASE AND ITS USES
; FILE REFERENCE: 00/21247
; CURRENT APPLICATION NUMBER: US/09/864,321
; CURRENT FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-864-321-2

Alignment Scores:

Pred. No.:	1.07e+03	Length:	24
Score:	40.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.40%	Indels:	0
DB:	9	Gaps:	0

US-09-899-440-18 (1-545) x US-09-864-321-2 (1-24)

```
Qy    118 SerTyrTrpGlnSerGlnVal 124
          |||||||||||||||||||||||
```

```
Db      22 AGTTACTGGCAATCTCAAGTC 2

RESULT 14
US-09-337-946A-12/c
; Sequence 12, Application US/09337946A
; Patent No. US20020164582A1
; GENERAL INFORMATION:
;  APPLICANT:  United States Army Medical Research Institute of
;  APPLICANT:  Infectious Diseases
;  APPLICANT:  Hart, Mary Katherine
;  APPLICANT:  Wilson, Julie A.
;  APPLICANT:  Pushko, Peter
;  APPLICANT:  Smith, Jonathan F.
;  APPLICANT:  Schmaljohn, Alan L.
;  TITLE OF INVENTION:  Ebola Virion Proteins Expressed from Venezuelan Equine Encephali
;  TITLE OF INVENTION:  Virus Replicons
;  FILE REFERENCE:  Army 144
;  CURRENT APPLICATION NUMBER: US/09/337,946A
;  CURRENT FILING DATE:  1999-06-22
;  PRIOR APPLICATION NUMBER:  US 60/091,403
;  PRIOR FILING DATE:  1998-06-29
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  IBM compatible, Word 97, Windows 95
; SEQ ID NO 12
;   LENGTH: 33
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: /note= "forward primer for VP35"
US-09-337-946A-12

Alignment Scores:
Pred. No.:                1.8e+03        Length:          33
Score:                    40.00          Matches:         7
Percent Similarity:       90.00%         Conservative:    2
Best Local Similarity:    70.00%         Mismatches:      1
Query Match:              1.40%          Indels:          0
DB:                       9              Gaps:            0

US-09-899-440-18 (1-545) x US-09-337-946A-12 (1-33)

Qy      52 HisLeuValSerProSerPheLeuSerVal 61
           |||||||||    |||:::|||||||||:::
Db      32 CATCTTGTTAGACCAGCTTTTCTATCGATC 3

RESULT 15
US-09-504-231A-2742/c
; Sequence 2742, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2742
;   LENGTH: 36
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid Mo
US-09-504-231A-2742

Alignment Scores:
Pred. No.:                2.07e+03       Length:          36
Score:                    40.00          Matches:         7
Percent Similarity:       83.33%         Conservative:    3
Best Local Similarity:    58.33%         Mismatches:      2
Query Match:              1.40%          Indels:          0
DB:                       10             Gaps:            0

US-09-899-440-18 (1-545) x US-09-504-231A-2742 (1-36)

Qy     483 ArgProLeuGlyProHisGlyLeuLeuSerLysSer 494
           ||||||      |||:::|||||||:::|||:::|||
Db      36 CGCCCCTTTCGGCCTAACGGCCTCATCAGCCGATCA 1


Search completed: January 10, 2003, 14:21:09
Job time : 77 secs
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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2003, 12:24:01 ; Search time 62 Seconds
(without alignments)
2695.788 Million cell updates/sec

Title: US-09-899-440-18
Perfect score: 2850
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 558892

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	53	1.9	24	2	US-08-922-170B-2	Sequence 2, Appli
c	2	53	1.9	24	2	US-08-922-170B-7	Sequence 7, Appli
c	3	53	1.9	24	4	US-09-071-739B-7	Sequence 7, Appli
c	4	47	1.6	36	2	US-08-863-639A-31	Sequence 31, Appl
	5	47	1.6	40	4	US-09-252-586-4	Sequence 4, Appli
c	6	46	1.6	32	4	US-09-260-038B-18	Sequence 18, Appl
c	7	46	1.6	32	4	US-09-635-923-18	Sequence 18, Appl
	8	43	1.5	35	4	US-09-252-586-10	Sequence 10, Appl
c	9	43	1.5	40	1	US-07-743-245-1	Sequence 1, Appli
c	10	41	1.4	39	3	US-08-448-619-2	Sequence 2, Appli
	11	41	1.4	39	3	US-08-448-619-3	Sequence 3, Appli
c	12	40	1.4	21	4	US-09-113-168-2	Sequence 2, Appli
	13	40	1.4	36	4	US-08-686-968C-128	Sequence 128, App
c	14	40	1.4	37	5	PCT-US94-10617-5	Sequence 5, Appli
c	15	39	1.4	24	3	US-08-393-157-1	Sequence 1, Appli
c	16	39	1.4	36	2	US-08-532-795-5	Sequence 5, Appli
	17	38	1.3	23	2	US-08-922-170B-6	Sequence 6, Appli
	18	38	1.3	23	4	US-09-071-739B-6	Sequence 6, Appli
	19	38	1.3	27	3	US-08-991-347-4	Sequence 4, Appli
c	20	38	1.3	28	4	US-09-260-038B-16	Sequence 16, Appl
c	21	38	1.3	28	4	US-09-635-923-16	Sequence 16, Appl
c	22	38	1.3	29	4	US-09-260-038B-22	Sequence 22, Appl
c	23	38	1.3	29	4	US-09-635-923-22	Sequence 22, Appl
	24	38	1.3	35	4	US-09-260-038B-6	Sequence 6, Appli
	25	38	1.3	35	4	US-09-635-923-6	Sequence 6, Appli
c	26	38	1.3	38	1	US-07-967-693-30	Sequence 30, Appl
c	27	38	1.3	38	1	US-08-195-072-28	Sequence 28, Appl
c	28	38	1.3	38	1	US-08-195-735-28	Sequence 28, Appl
c	29	38	1.3	38	1	US-08-195-747-28	Sequence 28, Appl
c	30	38	1.3	38	1	US-08-446-884-28	Sequence 28, Appl
c	31	38	1.3	38	1	US-08-195-073-28	Sequence 28, Appl
c	32	38	1.3	38	1	US-08-198-175-28	Sequence 28, Appl
c	33	38	1.3	38	2	US-08-443-153-28	Sequence 28, Appl
c	34	38	1.3	38	3	US-08-442-807-28	Sequence 28, Appl
c	35	38	1.3	39	5	PCT-US92-07916-8	Sequence 8, Appli
	36	38	1.3	39	5	PCT-US94-14106-21	Sequence 21, Appl
	37	37	1.3	21	4	US-09-252-586-12	Sequence 12, Appl
c	38	37	1.3	21	4	US-09-252-586-13	Sequence 13, Appl
c	39	37	1.3	30	4	US-09-674-460-2	Sequence 2, Appli
	40	37	1.3	35	4	US-09-255-368-26	Sequence 26, Appl
	41	37	1.3	35	4	US-09-260-038B-8	Sequence 8, Appli
	42	37	1.3	35	4	US-09-635-923-8	Sequence 8, Appli
c	43	37	1.3	36	1	US-08-525-058A-20	Sequence 20, Appl
	44	37	1.3	36	4	US-09-042-353-96	Sequence 96, Appl
	45	37	1.3	36	4	US-08-758-417A-360	Sequence 360, App

ALIGNMENTS

RESULT 1
US-08-922-170B-2/c
; Sequence 2, Application US/08922170B
; Patent No. 5968822
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
; APPLICANT: Feinstein
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
; TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
; TITLE OF INVENTION: SAME IN TRANSDUCED CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCI file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,170B
; FILING DATE: 2 SEP 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 910/1

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  972-3-5625553
;      TELEFAX:  972-3-5625554
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-922-170B-2
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Alignment Scores:

Pred. No.:	22.6	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	2	Gaps:	0

US-09-899-440-18 (1-545) x US-08-922-170B-2 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
```

```
RESULT 2
US-08-922-170B-7/c
; Sequence 7, Application US/08922170B
; Patent No. 5968822
;  GENERAL INFORMATION:
;    APPLICANT:  Iris Pecker, Israel Vlodavsky and Elena
;    APPLICANT:  Feinstein
;    TITLE OF INVENTION:  POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
;    TITLE OF INVENTION:  HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
;    TITLE OF INVENTION:  SAME IN TRANSDUCED CELLS
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark M. Friedman c/o Robert Sheinbein
;      STREET:  2940 Birchtree lane
;      CITY:  Silver Spring
;      STATE:  Maryland
;      COUNTRY:  United States of America
;      ZIP:  20906
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 megabyte, 3.5" microdisk
;      COMPUTER:  Twinhead* Slimnote-890TX
;      OPERATING SYSTEM:  MS DOS version 6.2,
;      OPERATING SYSTEM:  Windows version 3.11
;      SOFTWARE:  Word for Windows version 2.0 converted to
;      SOFTWARE:  an ASCI file
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/922,170B
;      FILING DATE:  2 SEP 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Friedmam, Mark M.
;      REGISTRATION NUMBER:  33,883
;      REFERENCE/DOCKET NUMBER:  910/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  972-3-5625553
;      TELEFAX:  972-3-5625554
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-922-170B-7
```

Alignment Scores:

Pred. No.:	22.6	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	2	Gaps:	0

US-09-899-440-18 (1-545) x US-08-922-170B-7 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
```

```
RESULT 3
US-09-071-739B-7/c
; Sequence 7, Application US/09071739B
; Patent No. 6177545
;  GENERAL INFORMATION:
;    APPLICANT:  Iris Pecker et al.
;    TITLE OF INVENTION:  HEPARANASE SPECIFIC MOLECULAR PROBES
;    TITLE OF INVENTION:  AND THEIR USE IN RESEARCH AND MEDICAL
;    TITLE OF INVENTION:  APPLICATIONS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark M. Friedman c/o Anthony Castorina
;      STREET:  20001 Jefferson Davis Highway, Suite 207
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  United States of America
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 megabyte, 3.5" microdisk
;      COMPUTER:  Twinhead* Slimnote-890TX
;      OPERATING SYSTEM:  MS DOS version 6.2,
;      OPERATING SYSTEM:  Windows version 3.11
;      SOFTWARE:  Word for Windows version 2.0 converted to
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,739B
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/922,180
;      FILING DATE:  September 2, 1997
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Friedmam, Mark M.
;      REGISTRATION NUMBER:  33,883
;      REFERENCE/DOCKET NUMBER:  910/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  972-3-5625553
;      TELEFAX:  972-3-5625554
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-071-739B-7
```

Alignment Scores:

Pred. No.:	22.6	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	4	Gaps:	0

US-09-899-440-18 (1-545) x US-09-071-739B-7 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1

RESULT 4
US-08-863-639A-31/c
; Sequence 31, Application US/08863639A
; Patent No. 5981185
;  GENERAL INFORMATION:
;    APPLICANT:  Matson, Robert S.
;    APPLICANT:  Coassin, Peter J.
;    APPLICANT:  Rampal, Jang B.
;    APPLICANT:  Caskey, C. T.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE REPEAT ARRAYS
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheldon & Mak
;      STREET:  225 South Lake Avenue, 9th Floor
;      CITY:  Pasadena
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Corel WordPerfect 8 version
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/863,639A
;      FILING DATE:  May 28, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Joseph E. Mueth
;      REGISTRATION NUMBER:  20,532
;      REFERENCE/DOCKET NUMBER:  11859-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (626) 796-4000
;      TELEFAX:  (626) 795-6321
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  36 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
US-08-863-639A-31

Alignment Scores:
Pred. No.:                252             Length:         36
Score:                    47.00           Matches:        9
Percent Similarity:       100.00%         Conservative:   1
Best Local Similarity:    90.00%          Mismatches:     0
Query Match:              1.65%           Indels:         0
DB:                       2               Gaps:           0

US-09-899-440-18 (1-545) x US-08-863-639A-31 (1-36)

Qy     10 ProProProLeuLeuMetLeuLeuLeuLeu 19
          ||||||||||||||:::|||||||||||
Db     34 CCGCCGCCGCTGCTGCTGCTGCTGCTGCTG 5

RESULT 5
US-09-252-586-4
; Sequence 4, Application US/09252586
; Patent No. 6387643
;  GENERAL INFORMATION:
;    APPLICANT:  Heinrikson, Robert L.
;    APPLICANT:  Fairbanks, Michael B.
;    APPLICANT:  Mildner, Ana M.
;    TITLE OF INVENTION:  Human Platelet Heparanase Polypeptides,
;    TITLE OF INVENTION:  Polynucleotide Molecules That Encode Them, and Methods For
;    TITLE OF INVENTION:  the Identification of Compounds That Alter Heparanase
;    TITLE OF INVENTION:  Activity
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pharmacia & Upjohn
;      STREET:  301 Henrietta
;      CITY:  Kalamazoo
;      STATE:  MI
;      COUNTRY:  USA
;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/252,586
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kerber, Lori L.
;      REGISTRATION NUMBER:  41,113
;      REFERENCE/DOCKET NUMBER:  6131.N CN1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616-833-0974
;      TELEFAX:  616-833-8897
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-252-586-4

Alignment Scores:
Pred. No.:                303             Length:         40
Score:                    47.00           Matches:        9
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              1.65%           Indels:         0
DB:                       4               Gaps:           0

US-09-899-440-18 (1-545) x US-09-252-586-4 (1-40)

Qy    160 LysLysPheLysAsnSerThrTyrSer 168
          |||||||||||||||||||||||||
Db     14 AAAAAGTTCAAGAACAGCACCTACTCA 40

RESULT 6
US-09-260-038B-18/c
; Sequence 18, Application US/09260038B
; Patent No. 6348344
;  GENERAL INFORMATION:
;       APPLICANT: Maty Ayal-Hershkovitz et al.
;       TITLE OF INVENTION: GENETICALLY MODIFIED CELLS AND METHODS FOR
;                           EXPRESSING RECOMBINANT HEPARANASE
;                           AND METHODS OF PURIFYING SAME
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;            STREET: 2001 Jefferson Davis Highway, Suite 207
;            CITY: Arlington
;            STATE: Virginia
;            COUNTRY: United States of America
;            ZIP: 22202
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;            COMPUTER: Twinhead* Slimnote-890TX
;            OPERATING SYSTEM: MS DOS version 6.2,
;                              Windows version 3.11
;            SOFTWARE: Word for Windows version 2.0 converted to
;                      an ASCI file
```

```
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/260,038B
;              FILING DATE: 02-Mar-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/071,618
;              FILING DATE: May 1, 1998
;              APPLICATION NUMBER: 09/071,739
;              FILING DATE: May 1, 1998
;              APPLICATION NUMBER: 08/922,180
;              FILING DATE: September 2, 1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Friedmam, Mark M.
;              REGISTRATION NUMBER: 33,883
;              REFERENCE/DOCKET NUMBER: 910/16
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 972-3-5625553
;              TELEFAX: 972-3-5625554
;              TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 18:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 32
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-260-038B-18

Alignment Scores:
Pred. No.:                272             Length:          32
Score:                    46.00           Matches:         8
Percent Similarity:       88.89%          Conservative:    0
Best Local Similarity:    88.89%          Mismatches:      1
Query Match:              1.61%           Indels:          0
DB:                       4               Gaps:            0

US-09-899-440-18 (1-545) x US-09-260-038B-18 (1-32)

Qy     114 PheGluGluArgSerTyrTrpGlnSer 122
           ||||||||||||||||||||    |||
Db      31 TTTGAAGAGAGAAGTTACTGGGCATCG 5

RESULT 7
US-09-635-923-18/c
; Sequence 18, Application US/09635923
; Patent No. 6426209
;   GENERAL INFORMATION:
;         APPLICANT: Maty Ayal-Hershkovitz et al.
;         TITLE OF INVENTION: GENETICALLY MODIFIED CELLS AND METHODS FOR
;                             EXPRESSING RECOMBINANT HEPARANASE
;                             AND METHODS OF PURIFYING SAME
;         NUMBER OF SEQUENCES: 25
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;              STREET: 2001 Jefferson Davis Highway, Suite 207
;              CITY: Arlington
;              STATE: Virginia
;              COUNTRY: United States of America
;              ZIP: 22202
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;              COMPUTER: PC
;              OPERATING SYSTEM: MS DOS version 6.2,
;                                Windows version 3.11
;              SOFTWARE: Word for Windows version 2.0 converted to       an ASCI file
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/635,923
;              FILING DATE: 10-Aug-2000
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/487,716
;              FILING DATE: 19-Jan-2000
;              APPLICATION NUMBER: 09/071,618
;              FILING DATE: May 1, 1998
;              APPLICATION NUMBER: 09/071,739
;              FILING DATE: May 1, 1998
;              APPLICATION NUMBER: 08/922,180
;              FILING DATE: September 2, 1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Friedmam, Mark M.
;              REGISTRATION NUMBER: 33,883
;              REFERENCE/DOCKET NUMBER: 910/16
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 972-3-5625553
;              TELEFAX: 972-3-5625554
;              TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 18:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 32
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-635-923-18

Alignment Scores:
Pred. No.:                272             Length:          32
Score:                    46.00           Matches:         8
Percent Similarity:       88.89%          Conservative:    0
Best Local Similarity:    88.89%          Mismatches:      1
Query Match:              1.61%           Indels:          0
DB:                       4               Gaps:            0

US-09-899-440-18 (1-545) x US-09-635-923-18 (1-32)

Qy     114 PheGluGluArgSerTyrTrpGlnSer 122
           ||||||||||||||||||||    |||
Db      31 TTTGAAGAGAGAAGTTACTGGGCATCG 5

RESULT 8
US-09-252-586-10
; Sequence 10, Application US/09252586
; Patent No. 6387643
;  GENERAL INFORMATION:
;    APPLICANT:  Heinrikson, Robert L.
;    APPLICANT:  Fairbanks, Michael B.
;    APPLICANT:  Mildner, Ana M.
;    TITLE OF INVENTION:  Human Platelet Heparanase Polypeptides,
;    TITLE OF INVENTION:  Polynucleotide Molecules That Encode Them, and Methods For
;    TITLE OF INVENTION:  the Identification of Compounds That Alter Heparanase
;    TITLE OF INVENTION:  Activity
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pharmacia & Upjohn
;      STREET:  301 Henrietta
;      CITY:  Kalamazoo
;      STATE:  MI
;      COUNTRY:  USA
;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/252,586
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kerber, Lori L.
;      REGISTRATION NUMBER:  41,113
;      REFERENCE/DOCKET NUMBER:  6131.N CN1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616-833-0974
;      TELEFAX:  616-833-8897
;  INFORMATION FOR SEQ ID NO:  10:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  35 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-252-586-10

Alignment Scores:
Pred. No.:              744          Length:        35
Score:                  43.00        Matches:       8
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            1.51%        Indels:        0
DB:                     4            Gaps:          0

US-09-899-440-18 (1-545) x US-09-252-586-10 (1-35)

Qy     160 LysLysPheLysAsnSerThrTyr 167
           |||||||||||||||||||||||
Db      12 AAAAAGTTCAAGAACAGCACCTAC 35

RESULT 9
US-07-743-245-1/c
; Sequence 1, Application US/07743245
; Patent No. 5279952
;  GENERAL INFORMATION:
;    APPLICANT:  Wu, Kun C.
;    TITLE OF INVENTION:  PCR-BASED STRATEGY OF CONSTRUCTING
;    TITLE OF INVENTION:  CHIMERIC DNA MOLECULES
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  750 Bering Drive, Suite 400
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  USA
;      ZIP:  77057
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/743,245
;      FILING DATE:  19910809
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniel, C. Steven
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-787-1400
;      TELEFAX:  713-789-2679
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    IMMEDIATE SOURCE:
;      CLONE:  HYPOTHETICAL SEQUENCE
US-07-743-245-1

Alignment Scores:
Pred. No.:              940          Length:        40
Score:                  43.00        Matches:       6
Percent Similarity:     84.62%       Conservative:  5
Best Local Similarity:  46.15%       Mismatches:    2
Query Match:            1.51%        Indels:        0
DB:                     1            Gaps:          0

US-09-899-440-18 (1-545) x US-07-743-245-1 (1-40)

Qy       7 ProAlaLeuProProProLeuLeuMetLeuLeuLeuLeu 19
             |||      |||||||||||||:::|||:::::::::::::
Db      39 CCTCCTCCTCCTCCTCCTCTGATGATGATGATGATGATG 1

RESULT 10
US-08-448-619-2/c
; Sequence 2, Application US/08448619
; Patent No. 6140059
;  GENERAL INFORMATION:
;    APPLICANT:  Schwallerr, Manfred
;    TITLE OF INVENTION:  METHOD FOR THE OBTENTION OF NATIVE
;    TITLE OF INVENTION:  DOMAINS OF VIRAL MEMBRANE PROTEINS, THEIR USE, ESPECIALLY
;    TITLE OF INVENTION:  AS VACCINE AGAINST HIV, AND THESE NATIVE DOMAINS OF VIRAL
;    TITLE OF INVENTION:  MEMBRANE PROTEINS THEMSELVES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hardaway Law Firm
;      STREET:  P.O. Box 10107 Federal Station
;      CITY:  Greenville
;      STATE:  SC
;      COUNTRY:  USA
;      ZIP:  29603-0107
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,619
;      FILING DATE:  29-SEP-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/DE94/00022
;      FILING DATE:  12-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 01 017.2
;      FILING DATE:  16-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hardaway III, John B.
;      REGISTRATION NUMBER:  26,554
;      REFERENCE/DOCKET NUMBER:  RPE-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  864-233-6700
;      TELEFAX:  864-233-2284
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
US-08-448-619-2

Alignment Scores:
Pred. No.:              1.59e+03     Length:        39
Score:                  41.00        Matches:       7
Percent Similarity:     87.50%       Conservative:  0
Best Local Similarity:  87.50%       Mismatches:    1
Query Match:            1.44%        Indels:        0
DB:                     3            Gaps:          0

US-09-899-440-18 (1-545) x US-08-448-619-2 (1-39)

Qy      20 GlyProLeuGlyProLeuSerPro 27
           |||||||||||||||||   |||
Db      37 GGTCCCCTTGGACCTCTTGGACCG 14

RESULT 11
US-08-448-619-3
; Sequence 3, Application US/08448619
; Patent No. 6140059
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Schwallerr, Manfred
;    TITLE OF INVENTION:  METHOD FOR THE OBTENTION OF NATIVE
;    TITLE OF INVENTION:  DOMAINS OF VIRAL MEMBRANE PROTEINS, THEIR USE, ESPECIALLY
;    TITLE OF INVENTION:  AS VACCINE AGAINST HIV, AND THESE NATIVE DOMAINS OF VIRAL
;    TITLE OF INVENTION:  MEMBRANE PROTEINS THEMSELVES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hardaway Law Firm
;      STREET:  P.O. Box 10107 Federal Station
;      CITY:  Greenville
;      STATE:  SC
;      COUNTRY:  USA
;      ZIP:  29603-0107
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,619
;      FILING DATE:  29-SEP-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/DE94/00022
;      FILING DATE:  12-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 01 017.2
;      FILING DATE:  16-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hardaway III, John B.
;      REGISTRATION NUMBER:  26,554
;      REFERENCE/DOCKET NUMBER:  RPE-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  864-233-6700
;      TELEFAX:  864-233-2284
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
US-08-448-619-3

Alignment Scores:
Pred. No.:                1.59e+03        Length:          39
Score:                    41.00           Matches:         7
Percent Similarity:       87.50%          Conservative:    0
Best Local Similarity:    87.50%          Mismatches:      1
Query Match:              1.44%           Indels:          0
DB:                       3               Gaps:            0

US-09-899-440-18 (1-545) x US-08-448-619-3 (1-39)

Qy      20 GlyProLeuGlyProLeuSerPro 27
           ||||||||||||||||||   |||
Db       7 GGTCCCCTTGGACCTCTTGGACCG 30

RESULT 12
US-09-113-168-2/c
; Sequence 2, Application US/09113168
; Patent No. 6190875
;   GENERAL INFORMATION:
;        APPLICANT: Hanna Ben-Artzi et al.
;        TITLE OF INVENTION: METHOD OF SCREENING FOR POTENTIAL ANTI-
;                            METASTATIC AND ANTI-INFLAMMATORY AGENTS USING
;                            MAMMALIAN HEPARANASE AS A PROBE
;        NUMBER OF SEQUENCES: 2
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;             STREET: 20001 Jefferson Davis Highway, Suite 207
;             CITY: Arlington
;             STATE: Virginia
;             COUNTRY: United States of America
;             ZIP: 22202
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;             COMPUTER: Twinhead* Slimnote-890TX
;             OPERATING SYSTEM: MS DOS version 6.2,
;                               Windows version 3.11
;             SOFTWARE: Word for Windows version 2.0 converted to
;                       an ASCI file
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/113,168
;             FILING DATE: 10-Jul-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/922,180
;             FILING DATE: September 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Friedmam, Mark M.
;             REGISTRATION NUMBER: 33,883
;             REFERENCE/DOCKET NUMBER: 910/8
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 972-3-5625553
;             TELEFAX: 972-3-5625554
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 21
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-113-168-2

Alignment Scores:
Pred. No.:                711             Length:          21
Score:                    40.00           Matches:         7
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              1.40%           Indels:          0
DB:                       4               Gaps:            0

US-09-899-440-18 (1-545) x US-09-113-168-2 (1-21)

Qy     362 AlaAlaGlyPheMetTrpLeu 368
           |||||||||||||||||||||
Db      21 GCAGCTGGCTTTATGTGGCTG 1

RESULT 13
US-08-686-968C-128
; Sequence 128, Application US/08686968C
; Patent No. 6221361
; GENERAL INFORMATION:
;  APPLICANT: Cochran, Mark D.
;  APPLICANT:  Junker, David E.
;  TITLE OF INVENTION: Recombinant Swinepox Virus
;  FILE REFERENCE: 39119-H/JML
;  CURRENT APPLICATION NUMBER: US/08/686,968C
;  CURRENT FILING DATE:  1996-07-25
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
;   LENGTH: 36
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Homology
;   OTHER INFORMATION: vector 779-94.31
US-08-686-968C-128

Alignment Scores:
Pred. No.:                1.83e+03        Length:          36
```

Score:	40.00	Matches:	7
Percent Similarity:	90.91%	Conservative:	3
Best Local Similarity:	63.64%	Mismatches:	1
Query Match:	1.40%	Indels:	0
DB:	4	Gaps:	0

US-09-899-440-18 (1-545) x US-08-686-968C-128 (1-36)

```
Qy    162 PheLysAsnSerThrTyrSerArgSerSerVal 172
          |||||||||:::|||||||   ||||||:::::
Db      2 TTTAAAAATACGACTTACTGCAGGTCGACTCTA 34
```

```
RESULT 14
PCT-US94-10617-5/c
; Sequence 5, Application PC/TUS9410617
;  GENERAL INFORMATION:
;    APPLICANT:  Bockman, Jeffrey M.
;    APPLICANT:  Drivas, George T.
;    APPLICANT:  Rush, Mark G.
;    APPLICANT:  Shih, Andy
;    TITLE OF INVENTION:  Ribozyme-Based Compositions for the Modification
;    TITLE OF INVENTION:  of Cutaneous Phenotypes associated with Aging
;    TITLE OF INVENTION:  and Other Conditions of the Skin and Hair
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Andy Shih
;      STREET:  30 Chestnut Drive
;      CITY:  Hastings-On-Hudson
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10706
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10617
;      FILING DATE:  15-SEP-1994
;      CLASSIFICATION:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-478-1911
;      TELEFAX:  212-750-3977
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  RNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  AATRZ1
PCT-US94-10617-5
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Alignment Scores:

Pred. No.:	1.92e+03	Length:	37
Score:	40.00	Matches:	7
Percent Similarity:	72.73%	Conservative:	1
Best Local Similarity:	63.64%	Mismatches:	3
Query Match:	1.40%	Indels:	0
DB:	5	Gaps:	0

US-09-899-440-18 (1-545) x PCT-US94-10617-5 (1-37)

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Qy    484 ProLeuGlyProHisGlyLeuLeuSerLysSer 494
          |||      ||||||||||||:::|||   |||
Db     34 CCATTTCGTCCTCACGGACTCATCAGCAACAGC 2
```

```
RESULT 15
US-08-393-157-1/c
; Sequence 1, Application US/08393157
; Patent No. 6080840
;  GENERAL INFORMATION:
;    APPLICANT:  Alfred E. Slanetz
;    APPLICANT:  Alfred L.M. Bothwell
;    TITLE OF INVENTION:  Soluble T Cell Receptors
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brumbaugh, Graves, Donohue & Raymond
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10112-0228
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette - 5.25 inch, 360 Kb
;      COMPUTER:  IBM XT Compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/393,157
;      FILING DATE:  17 February 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/822,538
;      FILING DATE:  17 January 1992
;      APPLICATION NUMBER:  08/168,782
;      FILING DATE:  14 December 1993
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 Nucleotides
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:
;    ANTI-SENSE:  No
;    IMMEDIATE SOURCE:
US-08-393-157-1
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Alignment Scores:

Pred. No.:	1.19e+03	Length:	24
Score:	39.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	1.37%	Indels:	0
DB:	3	Gaps:	0

US-09-899-440-18 (1-545) x US-08-393-157-1 (1-24)

```
Qy    293 AspSerValThrTrpHisHis 299
          ||||||   ||||||||||||
Db     22 GATTCGCGAACGTGGCATCAC 2
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Search completed: January 10, 2003, 14:19:39
Job time : 64 secs

GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2003, 12:22:52 ; Search time 4267 Seconds
(without alignments)
3717.138 Million cell updates/sec

Title: US-09-899-440-18
Perfect score: 2850
Sequence: 1 MLLRSKPALPPPLLMLLLLG.....LPAFSYSFFVIRNAKVAACI 545

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 774614

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09899440/runat_08012003_124403_23158/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=40
-USER=US09899440_@CGN_1_1_2586_@runat_08012003_124403_23158 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	53	1.9	24	6	AR080673	AR080673 Sequence
c 2	53	1.9	24	6	AR080678	AR080678 Sequence
c 3	53	1.9	24	6	AR125608	AR125608 Sequence
c 4	47	1.6	36	6	AR084542	AR084542 Sequence
5	47	1.6	40	6	AR210042	AR210042 Sequence
c 6	46	1.6	32	6	AR194203	AR194203 Sequence
7	43	1.5	35	6	AR210048	AR210048 Sequence
8	42	1.5	38	6	AX228017	AX228017 Sequence
c 9	42	1.5	40	6	E49126	E49126 Novel G pro
c 10	42	1.5	40	6	E50836	E50836 Novel G pro
c 11	41	1.4	39	6	AR116990	AR116990 Sequence
12	41	1.4	39	6	AR116991	AR116991 Sequence
13	41	1.4	40	6	AX033446	AX033446 Sequence
c 14	40	1.4	21	6	AR130850	AR130850 Sequence
15	40	1.4	36	6	AR147063	AR147063 Sequence
16	40	1.4	37	6	AX343802	AX343802 Sequence
17	40	1.4	38	6	AX218488	AX218488 Sequence
18	40	1.4	38	6	AX219627	AX219627 Sequence
19	40	1.4	38	6	AX219738	AX219738 Sequence
20	40	1.4	38	6	AX222547	AX222547 Sequence
21	40	1.4	38	6	AX222581	AX222581 Sequence
22	40	1.4	38	6	AX222637	AX222637 Sequence
23	40	1.4	38	6	AX227946	AX227946 Sequence
24	40	1.4	38	6	AX228234	AX228234 Sequence
25	40	1.4	38	6	AX228273	AX228273 Sequence
26	40	1.4	38	6	AX424787	AX424787 Sequence
c 27	39	1.4	24	6	AR100659	AR100659 Sequence
c 28	39	1.4	24	6	AX147949	AX147949 Sequence
29	39	1.4	31	6	AX248770	AX248770 Sequence
c 30	39	1.4	31	6	AX248796	AX248796 Sequence
c 31	39	1.4	36	6	A41187	A41187 Sequence 5
c 32	39	1.4	36	9	S73017	S73017 Homo sapien
33	39	1.4	38	6	AX222639	AX222639 Sequence
c 34	39	1.4	40	6	AX428592	AX428592 Sequence
35	38	1.3	23	6	AR080677	AR080677 Sequence
36	38	1.3	23	6	AR125607	AR125607 Sequence
37	38	1.3	27	6	A91900	A91900 Sequence 4
38	38	1.3	27	6	AR106366	AR106366 Sequence
39	38	1.3	27	6	AX032403	AX032403 Sequence
40	38	1.3	27	13	AX032409	AX032409 Sequence
c 41	38	1.3	28	6	AR194201	AR194201 Sequence
c 42	38	1.3	29	6	AR194207	AR194207 Sequence
43	38	1.3	35	6	AR194193	AR194193 Sequence
c 44	38	1.3	35	6	AX015343	AX015343 Sequence
c 45	38	1.3	38	6	A13910	A13910 Nucleotide

ALIGNMENTS

RESULT 1

```
AR080673/c
LOCUS       AR080673                 24 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 2 from patent US 5968822.
ACCESSION   AR080673
VERSION     AR080673.1  GI:10007403
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in transduced cells
  JOURNAL   Patent: US 5968822-A 2 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        7 a      4 c      6 g      7 t
ORIGIN

Alignment Scores:
Pred. No.:                1.22e+03        Length:          24
Score:                    53.00           Matches:         8
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              1.86%           Indels:          0
DB:                       6               Gaps:            0

US-09-899-440-18 (1-545) x AR080673 (1-24)

Qy     293 AspSerValThrTrpHisHisTyr 300
           ||||||||||||||||||||||||
Db      24 GATTCAGTTACATGGCATCACTAC 1

RESULT 2
AR080678/c
LOCUS       AR080678                 24 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 7 from patent US 5968822.
ACCESSION   AR080678
VERSION     AR080678.1  GI:10007408
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in transduced cells
  JOURNAL   Patent: US 5968822-A 7 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        7 a      4 c      6 g      7 t
ORIGIN

Alignment Scores:
Pred. No.:                1.22e+03        Length:          24
Score:                    53.00           Matches:         8
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              1.86%           Indels:          0
DB:                       6               Gaps:            0

US-09-899-440-18 (1-545) x AR080678 (1-24)

Qy     293 AspSerValThrTrpHisHisTyr 300
           ||||||||||||||||||||||||
Db      24 GATTCAGTTACATGGCATCACTAC 1

RESULT 3
AR125608/c
LOCUS       AR125608                 24 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 7 from patent US 6177545.
ACCESSION   AR125608
VERSION     AR125608.1  GI:14111670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Pecker,I., Vlodavsky,I., Friedman,Y. and Perets,T.
  TITLE     Heparanase specific molecular probes and their use in research and
            medical applications
  JOURNAL   Patent: US 6177545-A 7 23-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT        7 a      4 c      6 g      7 t
ORIGIN

Alignment Scores:
Pred. No.:                1.22e+03        Length:          24
Score:                    53.00           Matches:         8
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              1.86%           Indels:          0
DB:                       6               Gaps:            0

US-09-899-440-18 (1-545) x AR125608 (1-24)

Qy     293 AspSerValThrTrpHisHisTyr 300
           ||||||||||||||||||||||||
Db      24 GATTCAGTTACATGGCATCACTAC 1

RESULT 4
AR084542/c
LOCUS       AR084542                 36 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 31 from patent US 5981185.
ACCESSION   AR084542
VERSION     AR084542.1  GI:10011313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 31 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="unknown"
BASE COUNT        8 a      12 c     16 g      0 t
ORIGIN

Alignment Scores:
Pred. No.:                7.16e+03        Length:          36
Score:                    47.00           Matches:         9
Percent Similarity:       100.00%         Conservative:    1
Best Local Similarity:    90.00%          Mismatches:      0
Query Match:              1.65%           Indels:          0
DB:                       6               Gaps:            0

US-09-899-440-18 (1-545) x AR084542 (1-36)

Qy      10 ProProProLeuLeuMetLeuLeuLeuLeu 19
           ||||||||||||||:::|||||||||||||
Db      34 CCGCCGCCGCTGCTGCTGCTGCTGCTGCTG 5

RESULT 5
AR210042
LOCUS       AR210042                 40 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6387643.
ACCESSION   AR210042
VERSION     AR210042.1  GI:21512169
KEYWORDS    .
SOURCE      Unknown.
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Heinrikson,R.Leroy., Fairbanks,M.B. and Mildner,A.M.
  TITLE     Human platelet heparanase polypeptides, polynucleotide molecules
            that encode them, and methods for the identification of compounds
            that alter heparanase activity
  JOURNAL   Patent: US 6387643-A 4 14-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
BASE COUNT       16 a      10 c       7 g       7 t
ORIGIN

Alignment Scores:
Pred. No.:                 8.26e+03        Length:          40
Score:                     47.00           Matches:         9
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               1.65%           Indels:          0
DB:                        6               Gaps:            0

US-09-899-440-18 (1-545) x AR210042 (1-40)

Qy    160 LysLysPheLysAsnSerThrTyrSer 168
          |||||||||||||||||||||||||||
Db     14 AAAAAGTTCAAGAACAGCACCTACTCA 40

RESULT 6
AR194203/c
LOCUS       AR194203                  32 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 18 from patent US 6348344.
ACCESSION   AR194203
VERSION     AR194203.1  GI:20240795
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Ayal-Hershkovitz,M., Moskowitz,H., Miron,D., Gilboa,A., Mimon,M.,
            Ben-Artzi,H., Yacoby-Zeevi,O., Pecker,I., Peleg,Y. and Schlomi,Y.
  TITLE     Genetically modified cells and methods for expressing recombinant
            heparanase and methods of purifying same
  JOURNAL   Patent: US 6348344-A 18 19-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
BASE COUNT        8 a      11 c       4 g       9 t
ORIGIN

Alignment Scores:
Pred. No.:                 7.47e+03        Length:          32
Score:                     46.00           Matches:         8
Percent Similarity:        88.89%          Conservative:    0
Best Local Similarity:     88.89%          Mismatches:      1
Query Match:               1.61%           Indels:          0
DB:                        6               Gaps:            0

US-09-899-440-18 (1-545) x AR194203 (1-32)

Qy    114 PheGluGluArgSerTyrTrpGlnSer 122
          |||||||||||||||||||||  |||
Db     31 TTTGAAGAGAGAAGTTACTGGGCATCG 5

RESULT 7
AR210048
LOCUS       AR210048                  35 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 10 from patent US 6387643.
ACCESSION   AR210048
VERSION     AR210048.1  GI:21512177
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Heinrikson,R.Leroy., Fairbanks,M.B. and Mildner,A.M.
  TITLE     Human platelet heparanase polypeptides, polynucleotide molecules
            that encode them, and methods for the identification of compounds
            that alter heparanase activity
  JOURNAL   Patent: US 6387643-A 10 14-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT       15 a       8 c       6 g       6 t
ORIGIN

Alignment Scores:
Pred. No.:                 1.55e+04        Length:          35
Score:                     43.00           Matches:         8
Percent Similarity:        100.00%         Conservative:    0
Best Local Similarity:     100.00%         Mismatches:      0
Query Match:               1.51%           Indels:          0
DB:                        6               Gaps:            0

US-09-899-440-18 (1-545) x AR210048 (1-35)

Qy    160 LysLysPheLysAsnSerThrTyr 167
          |||||||||||||||||||||||
Db     12 AAAAAGTTCAAGAACAGCACCTAC 35

RESULT 8
AX228017
LOCUS       AX228017                  38 bp    mRNA    linear   PAT 10-SEP-2001
DEFINITION  Sequence 1389 from Patent WO0157206.
ACCESSION   AX228017
VERSION     AX228017.1  GI:15557158
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 1389 09-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        9 a       7 c      14 g       8 t
ORIGIN

Alignment Scores:
Pred. No.:                 2.12e+04        Length:          38
Score:                     42.00           Matches:         8
Percent Similarity:        81.82%          Conservative:    1
Best Local Similarity:     72.73%          Mismatches:      2
Query Match:               1.47%           Indels:          0
DB:                        6               Gaps:            0

US-09-899-440-18 (1-545) x AX228017 (1-38)

Qy    480 TyrLeuLeuArgProLeuGlyProHisGlyLeu 490
          |||||||:::|||||||||||||      ||||||
Db      6 TATCTGATGAGGCCGTTAGGCCGAAAGGGGCTG 38

RESULT 9
E49126/c
LOCUS       E49126                    40 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-conjugated receptor protein.
ACCESSION   E49126
VERSION     E49126.1  GI:18629263
KEYWORDS    JP 2001029083-A/4.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Takasaki,A., Matsumoto,M., Sugimoto,T., Kamahara,M. and Saito,S.
  TITLE     Novel G protein-conjugated receptor protein
  JOURNAL   Patent: JP 2001029083-A 4 06-FEB-2001;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001029083-A/4
            PD   06-FEB-2001
            PF   23-JUL-1999 JP 1999209918
            PR
            PI   ATSUSHI TAKASAKI,MITSUYUKI MATSUMOTO,TAKASHI SUGIMOTO, PI
            MASAZUMI KAMAHARA,
            PI   SATOSHI SAITO
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61P25/04,
            PC   A61P25/16,
            PC   A61P25/18,C07K14/705,C12N5/10,C12P21/02,C12P21/08,C12Q1/68, PC
              G01N33/15,
            PC   G01N33/50,G01N33/53,G01N33/566,C12N15/00,A61K37/02,C12N5/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .40
            FT                   /organism='Homo sapiens (human)'.
FEATURES                Location/Qualifiers
     source             1. .40
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT         10 a       8 c       4 g       18 t
ORIGIN

Alignment Scores:
Pred. No.:                  2.27e+04        Length:         40
Score:                      42.00           Matches:        7
Percent Similarity:         92.31%          Conservative:   5
Best Local Similarity:      53.85%          Mismatches:     1
Query Match:                1.47%           Indels:         0
DB:                         6               Gaps:           0

US-09-899-440-18 (1-545) x E49126 (1-40)

Qy      72 ArgPheLeuIleLeuLeuGlySerProLysLeuArgThr 84
           :::::::::|||||||:::   ||||||||||:::|||||||
Db      40 AAGTATATGATTCTTATAGAAAGTCCAAAAGTAAGGACA 2

RESULT 10
E50836/c
LOCUS       E50836                    40 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor.
ACCESSION   E50836
VERSION     E50836.1  GI:18633541
KEYWORDS    JP 2001054389-A/4.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Takasaki,A., Matsumoto,M., Sugimoto,T., Kamahara,M. and Saito,S.
  TITLE     Novel G protein-coupled receptor
  JOURNAL   Patent: JP 2001054389-A 4 27-FEB-2001;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001054389-A/4
            PD   27-FEB-2001
            PF   17-AUG-1999 JP 1999230777
            PR
            PI   ATSUSHI TAKASAKI,MITSUYUKI MATSUMOTO,TAKASHI SUGIMOTO, PI
            MASAZUMI KAMAHARA,
            PI   SATOSHI SAITO
            PC   C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,G01N33/15,G01N33/50//C12P21/08,(C12P21/02,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00
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            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES                Location/Qualifiers
     source             1. .40
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
BASE COUNT         10 a       8 c       4 g       18 t
ORIGIN

Alignment Scores:
Pred. No.:                  2.27e+04        Length:         40
Score:                      42.00           Matches:        7
Percent Similarity:         92.31%          Conservative:   5
Best Local Similarity:      53.85%          Mismatches:     1
Query Match:                1.47%           Indels:         0
DB:                         6               Gaps:           0

US-09-899-440-18 (1-545) x E50836 (1-40)

Qy      72 ArgPheLeuIleLeuLeuGlySerProLysLeuArgThr 84
           :::::::::|||||||:::   ||||||||||:::|||||||
Db      40 AAGTATATGATTCTTATAGAAAGTCCAAAAGTAAGGACA 2

RESULT 11
AR116990/c
LOCUS       AR116990                  39 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6140059.
ACCESSION   AR116990
VERSION     AR116990.1  GI:14097896
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Schawaller,M.
  TITLE     Methods for the obtention of human immunodeficiency virsus Type 1
            envelope glycoproteins in native and oligomeric form employing
            recombinant chimeric antigens containing collagenase recognition
            sites
  JOURNAL   Patent: US 6140059-A 2 31-OCT-2000;
FEATURES                Location/Qualifiers
     source             1. .39
                        /organism="unknown"
BASE COUNT         10 a       10 c      12 g       7 t
ORIGIN

Alignment Scores:
Pred. No.:                  2.69e+04        Length:         39
Score:                      41.00           Matches:        7
Percent Similarity:         87.50%          Conservative:   0
Best Local Similarity:      87.50%          Mismatches:     1
Query Match:                1.44%           Indels:         0
DB:                         6               Gaps:           0

US-09-899-440-18 (1-545) x AR116990 (1-39)

Qy      20 GlyProLeuGlyProLeuSerPro 27
           |||||||||||||||||||   |||
Db      37 GGTCCCCTTGGACCTCTTGGACCG 14

RESULT 12
AR116991
LOCUS       AR116991                  39 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6140059.
ACCESSION   AR116991
VERSION     AR116991.1  GI:14097897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Schawaller,M.
  TITLE     Methods for the obtention of human immunodeficiency virsus Type 1
            envelope glycoproteins in native and oligomeric form employing
            recombinant chimeric antigens containing collagenase recognition
            sites
  JOURNAL   Patent: US 6140059-A 3 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="unknown"
BASE COUNT        7 a      12 c      10 g      10 t
ORIGIN

Alignment Scores:
Pred. No.:              2.69e+04        Length:         39
Score:                  41.00           Matches:        7
Percent Similarity:     87.50%          Conservative:   0
Best Local Similarity:  87.50%          Mismatches:     1
Query Match:            1.44%           Indels:         0
DB:                     6               Gaps:           0

US-09-899-440-18 (1-545) x AR116991 (1-39)

Qy      20 GlyProLeuGlyProLeuSerPro 27
           |||||||||||||||||   |||
Db       7 GGTCCCCTTGGACCTCTTGGACCG 30

RESULT 13
AX033446
LOCUS       AX033446                 40 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 27 from Patent WO0044896.
ACCESSION   AX033446
VERSION     AX033446.1  GI:10280207
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Beyaert,R. and Cornelis,S.
  TITLE     Internal ribosome entry site (ires), vector containing same and
            uses thereof
  JOURNAL   Patent: WO 0044896-A 27 03-AUG-2000;
            VLAAMS INTERUNIV INST BIOTECH (BE) ; BEYAERT RUDI (BE) ; CORNELIS
            SIGRID (BE)
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="E-tag probe"
BASE COUNT        6 a      15 c      13 g      6 t
ORIGIN

Alignment Scores:
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Score:                  41.00           Matches:        7
Percent Similarity:     66.67%          Conservative:   1
Best Local Similarity:  58.33%          Mismatches:     4
Query Match:            1.44%           Indels:         0
DB:                     6               Gaps:           0

US-09-899-440-18 (1-545) x AX033446 (1-40)

Qy     344 GlyGluThrSerSerAlaTyrGlyGlyGlyAlaPro 355
           |||   :::   |||   ||||||   |||||||||
Db       5 GGTTCCAGCGGATCCGGATACGGCTCCGGCGCACCT 40

RESULT 14
AR130850/c
LOCUS       AR130850                 21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6190875.
ACCESSION   AR130850
VERSION     AR130850.1  GI:14119175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ben-Artzi,H., Ayal-Hershkovitz,M., Vlodavsky,I., Pecker,I.,
            Peleg,Y. and Miron,D.
  TITLE     Method of screening for potential anti-metastatic and
            anti-inflammatory agents using mammalian heparanase as a probe
  JOURNAL   Patent: US 6190875-A 2 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        7 a      8 c      4 g      2 t
ORIGIN

Alignment Scores:
Pred. No.:              1.42e+04        Length:         21
Score:                  40.00           Matches:        7
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            1.40%           Indels:         0
DB:                     6               Gaps:           0

US-09-899-440-18 (1-545) x AR130850 (1-21)

Qy     362 AlaAlaGlyPheMetTrpLeu 368
           |||||||||||||||||||||
Db      21 GCAGCTGGCTTTATGTGGCTG 1

RESULT 15
AR147063
LOCUS       AR147063                 36 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 128 from patent US 6221361.
ACCESSION   AR147063
VERSION     AR147063.1  GI:15110866
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Cochran,M.D. and Junker,D.E.
  TITLE     Recombinant swinepox virus
  JOURNAL   Patent: US 6221361-A 128 24-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="unknown"
BASE COUNT       12 a      7 c      6 g      11 t
ORIGIN

Alignment Scores:
Pred. No.:              2.95e+04        Length:         36
Score:                  40.00           Matches:        7
Percent Similarity:     90.91%          Conservative:   3
Best Local Similarity:  63.64%          Mismatches:     1
Query Match:            1.40%           Indels:         0
DB:                     6               Gaps:           0

US-09-899-440-18 (1-545) x AR147063 (1-36)

Qy     162 PheLysAsnSerThrTyrSerArgSerSerVal 172
           |||||||||:::|||||||   |||||||::::::
Db       2 TTTAAAAATACGACTTACTGCAGGTCGACTCTA 34


Search completed: January 10, 2003, 13:41:54
Job time : 4269 secs
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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2003, 11:16:56 ; Search time 312 Seconds
(without alignments)
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Title: US-09-899-440-18
Perfect score: 2850
Sequence: 1 MLLRSKPALPPPLLMLLLLG.....LPAFSYSFFVIRNAKVAACI 545

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	53	1.9	24	20	AAX35643	PCR primer used to
c	2	53	1.9	24	20	AAX35647	PCR primer used to
c	3	53	1.9	24	21	AAA75045	PCR primer HPL229
c	4	53	1.9	24	21	AAA75050	PCR primer HPL229
c	5	53	1.9	24	21	AAA75067	PCR primer Hpl 229
c	6	53	1.9	24	21	AAZ33294	Human heparanase P
	7	47	1.6	30	24	ABN86005	Human heparanase g
	8	47	1.6	40	20	AAZ11239	PCR primer for hum
c	9	46	1.6	32	21	AAZ47781	Heparanase express
	10	43	1.5	25	22	AAI67044	Human heparanase-1
	11	43	1.5	35	20	AAZ11243	PCR primer for hum
c	12	43	1.5	40	15	AAQ55601	Flanking sequences
	13	42	1.5	38	22	AAH96175	Human Chk1 ribozym
c	14	42	1.5	40	22	AAF81504	Novel human G prot
c	15	42	1.5	40	22	AAF87604	DNA associated wit
	16	41	1.4	24	21	AAC58530	Human PRO4333 (UNQ
	17	41	1.4	29	24	ABK33817	S. pneumoniae BVH-
	18	41	1.4	40	21	AAA73735	E-tag probe used t
	19	41	1.4	40	24	ABL51648	E-tag probe SEQ ID
c	20	40	1.4	21	21	AAZ88836	Human heparanase P
c	21	40	1.4	24	24	ABK52391	Embryo implantatio
c	22	40	1.4	33	21	AAZ87200	Ebola virus struct
	23	40	1.4	36	22	AAS11862	Human collagen gen
c	24	40	1.4	37	14	AAQ37184	Ribozyme gene inse
c	25	40	1.4	37	16	AAQ83545	Elastase target mR
	26	40	1.4	37	20	AAX91981	Porphorymonas ging
	27	40	1.4	37	24	ABL53027	Oligonucleotide JC
	28	40	1.4	38	22	AAH96104	Human Chk1 ribozym
	29	40	1.4	38	22	AAH96392	Human Chk1 ribozym
	30	40	1.4	38	22	AAH96431	Human Chk1 ribozym
	31	40	1.4	38	23	ABK03930	Human NOGO Hammerh
	32	40	1.4	38	23	ABK05069	Human NOGO Inozyme
	33	40	1.4	38	23	ABK05180	Human NOGO Inozyme
	34	40	1.4	38	23	ABK07989	Human CD20 Hammerh
	35	40	1.4	38	23	ABK08023	Human CD20 Hammerh
	36	40	1.4	38	23	ABK08079	Human CD20 Hammerh
	37	40	1.4	38	24	ABK58424	Human CLCA1 gene e
	38	40	1.4	38	24	ABK20476	Human ERG inozyme,
c	39	40	1.4	40	21	AAZ95991	Polynucleotide seq
	40	40	1.4	40	22	AAF55862	Tryptophanyl-tRNA
c	41	39	1.4	24	21	AAA62949	Chimeric alpha TCR
c	42	39	1.4	24	22	AAH20942	Human heparanase i
	43	39	1.4	30	24	ABN86004	Human heparanase g
	44	39	1.4	31	22	AAI30361	Human single nucle
c	45	39	1.4	31	22	AAI30387	Human single nucle

ALIGNMENTS

RESULT 1
AAX35643/c
ID AAX35643 standard; DNA; 24 BP.
XX
AC AAX35643;
XX
DT 09-JUL-1999 (first entry)
XX
DE PCR primer used to amplify human hp3 cDNA.
XX
KW Heparanase; hp; modulator; heparin-binding growth factor;
KW cellular response; cytokine; cell interaction; plasma lipoprotein;
KW cellular susceptibility; infection; disintegration;
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
KW atherscleros is; inflammation; neurodegenerative disease; neutralise;
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure;
KW PCR primer; ss.
XX

```
OS   Synthetic.
XX
PN   WO9911798-A1.
XX
PD   11-MAR-1999.
XX
PF   31-AUG-1998;   98WO-US17954.
XX
PR   02-JUL-1998;   98US-0109386.
PR   02-SEP-1997;   97US-0922170.
XX
PA   (FRIE/) FRIEDMAN M M.
PA   (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA   (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX
PI   Feinstein E,  Pecker I,  Vlodavsky I;
XX
DR   WPI; 1999-302255/25.
XX
PT   New human polynucleotide useful for treating angiogenesis,
PT   restenosis, and inflammation
XX
PS   Example 1; Page 22; 63pp; English.
XX
CC   The specification describes a polypeptide having heparanase (hp)
CC   activity. The recombinant protein is used as a modulator of
CC   heparin-binding growth factors, cellular responses to heparin-binding
CC   growth factors and cytokines, cell interaction with plasma lipoproteins,
CC   cellular susceptibility to viral, protozoal and bacterial infections
CC   or disintegration of neurodegenerative plaques. Heparanase may be
CC   useful for conditions such as wound healing, angiogenesis, restenosis,
CC   atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC   infections. Mammalian heparanase can be used to neutralize plasma
CC   heparin, and anti-heparanase antibodies may be applied for
CC   immunodetection and diagnosis of micrometastases, autoimmune lesions,
CC   and renal failure in biopsy specimens, plasma samples, and body fluids.
CC   PCR primers AAX35642-43 were used to amplify hp3 cDNA, in the course of
CC   the invention.
XX
SQ   Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:                439          Length:         24
Score:                    53.00        Matches:        8
Percent Similarity:       100.00%      Conservative:   0
Best Local Similarity:    100.00%      Mismatches:     0
Query Match:              1.86%        Indels:         0
DB:                       20           Gaps:           0

US-09-899-440-18 (1-545) x AAX35643 (1-24)

Qy     293 AspSerValThrTrpHisHisTyr 300
           ||||||||||||||||||||||||
Db      24 GATTCAGTTACATGGCATCACTAC 1

RESULT 2
AAX35647/c
ID   AAX35647 standard; DNA; 24 BP.
XX
AC   AAX35647;
XX
DT   09-JUL-1999  (first entry)
XX
DE   PCR primer used to amplify human hp3 cDNA.
XX
KW   Heparanase; hp; modulator; heparin-binding growth factor;
KW   cellular response; cytokine; cell interaction; plasma lipoprotein;
KW   cellular susceptibility; infection; disintegration;
KW   neurodegenerative plaque; wound healing; angiogenesis; restenosis;
KW   atherosclerosis; inflammation; neurodegenerative disease; neutralise;
KW   plasma heparin; micrometastasis; autoimmune lesion; renal failure;
KW   PCR primer; ss.
XX
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OS   Synthetic.
XX
PN   WO9911798-A1.
XX
PD   11-MAR-1999.
XX
PF   31-AUG-1998;   98WO-US17954.
XX
PR   02-JUL-1998;   98US-0109386.
PR   02-SEP-1997;   97US-0922170.
XX
PA   (FRIE/) FRIEDMAN M M.
PA   (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA   (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX
PI   Feinstein E,  Pecker I,  Vlodavsky I;
XX
DR   WPI; 1999-302255/25.
XX
PT   New human polynucleotide useful for treating angiogenesis,
PT   restenosis, and inflammation
XX
PS   Example 1; Page 23; 63pp; English.
XX
CC   The specification describes a polypeptide having heparanase (hp)
CC   activity. The recombinant protein is used as a modulator of
CC   heparin-binding growth factors, cellular responses to heparin-binding
CC   growth factors and cytokines, cell interaction with plasma lipoproteins,
CC   cellular susceptibility to viral, protozoal and bacterial infections
CC   or disintegration of neurodegenerative plaques. Heparanase may be
CC   useful for conditions such as wound healing, angiogenesis, restenosis,
CC   atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC   infections. Mammalian heparanase can be used to neutralize plasma
CC   heparin, and anti-heparanase antibodies may be applied for
CC   immunodetection and diagnosis of micrometastases, autoimmune lesions,
CC   and renal failure in biopsy specimens, plasma samples, and body fluids.
CC   PCR primers AAX35646-47 were used to amplify hp3 cDNA, in the course of
CC   the invention.
XX
SQ   Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:                439          Length:         24
Score:                    53.00        Matches:        8
Percent Similarity:       100.00%      Conservative:   0
Best Local Similarity:    100.00%      Mismatches:     0
Query Match:              1.86%        Indels:         0
DB:                       20           Gaps:           0

US-09-899-440-18 (1-545) x AAX35647 (1-24)

Qy     293 AspSerValThrTrpHisHisTyr 300
           ||||||||||||||||||||||||
Db      24 GATTCAGTTACATGGCATCACTAC 1

RESULT 3
AAA75045/c
ID   AAA75045 standard; DNA; 24 BP.
XX
AC   AAA75045;
XX
DT   15-JAN-2001  (first entry)
XX
DE   PCR primer HPL229 used to amplify human cDNA encoding heparanase.
XX
KW   Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW   heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW   wound healing; infection; burn; angiogenesis; restenosis;
KW   atherosclerosis; inflammation; neurodegenerative disease;
KW   Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
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PN WO200052178-A1.
XX
PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000WO-US03542.
XX
PR 01-MAR-1999; 99US-0258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2000-579289/54.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumour, inflammation, autoimmunity, neurodegenerative diseases -
XX
PS Disclosure; Page 44; 152pp; English.
XX
CC The present PCR primer was used to amplify a human cDNA sequence,
CC which encoded a protein with heparanase catalytic activity. The
CC heparanase (hpa) polynucleotide is useful in gene therapy, particularly
CC in treating tumour, inflammation or autoimmunity. Particularly, the
CC polynucleotide is useful in modulating the bioavailability of
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors (e.g. bFGF) and cytokines (e.g. interleukin (IL)-8),
CC cell interaction with plasma lipoproteins, cellular susceptibility to
CC certain viral and some bacterial and protozoa infections, or
CC disintegration of neurodegenerative plaques. The polynucleotide is
CC also useful in wound healing (e.g. thermal, chemical or radiation burns),
CC and in the treatment of angiogenesis, restenosis, atherosclerosis,
CC inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome
CC or Creutzfeldt-Jakob disease), and some viral, bacterial or protozoa
CC infections.
XX
SQ Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	439	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	21	Gaps:	0

US-09-899-440-18 (1-545) x AAA75045 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
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RESULT 4
AAA75050/c
ID AAA75050 standard; DNA; 24 BP.
XX
AC AAA75050;
XX
DT 15-JAN-2001 (first entry)
XX
DE PCR primer HPL229 used to amplify human cDNA encoding heparanase.
XX
KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200052178-A1.
XX
PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000WO-US03542.
XX
PR 01-MAR-1999; 99US-0258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2000-579289/54.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumour, inflammation, autoimmunity, neurodegenerative diseases -
XX
PS Disclosure; Page 44; 152pp; English.
XX
CC The present PCR primer was used to amplify a human cDNA sequence,
CC which encoded a protein with heparanase catalytic activity. The
CC heparanase (hpa) polynucleotide is useful in gene therapy, particularly
CC in treating tumour, inflammation or autoimmunity. Particularly, the
CC polynucleotide is useful in modulating the bioavailability of
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors (e.g. bFGF) and cytokines (e.g. interleukin (IL)-8),
CC cell interaction with plasma lipoproteins, cellular susceptibility to
CC certain viral and some bacterial and protozoa infections, or
CC disintegration of neurodegenerative plaques. The polynucleotide is
CC also useful in wound healing (e.g. thermal, chemical or radiation burns),
CC and in the treatment of angiogenesis, restenosis, atherosclerosis,
CC inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome
CC or Creutzfeldt-Jakob disease), and some viral, bacterial or protozoa
CC infections.
XX
SQ Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	439	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	21	Gaps:	0

US-09-899-440-18 (1-545) x AAA75050 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
```

RESULT 5
AAA75067/c
ID AAA75067 standard; DNA; 24 BP.
XX
AC AAA75067;
XX
DT 15-JAN-2001 (first entry)
XX
DE PCR primer Hpl 229 used to amplify human cDNA encoding heparanase.
XX
KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200052178-A1.
XX

PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000WO-US03542.
XX
PR 01-MAR-1999; 99US-0258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2000-579289/54.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumour, inflammation, autoimmunity, neurodegenerative diseases -
XX
PS Disclosure; Page 45; 152pp; English.
XX
CC The present PCR primer was used to amplify a human cDNA sequence,
CC which encoded a protein with heparanase catalytic activity. The
CC heparanase (hpa) polynucleotide is useful in gene therapy, particularly
CC in treating tumour, inflammation or autoimmunity. Particularly, the
CC polynucleotide is useful in modulating the bioavailability of
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors (e.g. bFGF) and cytokines (e.g. interleukin (IL)-8),
CC cell interaction with plasma lipoproteins, cellular susceptibility to
CC certain viral and some bacterial and protozoa infections, or
CC disintegration of neurodegenerative plaques. The polynucleotide is
CC also useful in wound healing (e.g. thermal, chemical or radiation burns),
CC and in the treatment of angiogenesis, restenosis, atherosclerosis,
CC inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome
CC or Creutzfeldt-Jakob disease), and some viral, bacterial or protozoa
CC infections.
XX
SQ Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	439	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	21	Gaps:	0

US-09-899-440-18 (1-545) x AAA75067 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
```

RESULT 6
AAZ33294/c
ID AAZ33294 standard; DNA; 24 BP.
XX
AC AAZ33294;
XX
DT 21-FEB-2000 (first entry)
XX
DE Human heparanase PCR primer Hpl-229 SEQ ID NO:7.
XX
KW Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
KW antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;
KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
KW inflammation; haemorrhagic nephritis; nephrotic syndrome;
KW autoimmune disease; anticancer; kidney disease; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9957153-A1.

XX
PD 11-NOV-1999.
XX
PF 28-APR-1999; 99WO-US09255.
XX
PR 01-MAY-1998; 98US-0071739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Friedman Y, Perets T;
XX
DR WPI; 2000-052944/04.
XX
PT Heparanase-specific molecular probes useful for diagnosis and
PT treatment, e.g. of tumors, and for targeted drug delivery -
XX
PS Example; Page 30; 90pp; English.
XX
CC The present invention describes heparanase-specific molecular probes,
CC useful for methods of detecting heparanase in situ. The probes and
CC anti-heparanase antibodies are used to detect or quantify the expression
CC of heparanase, for diagnosis and monitoring of diseases (especially
CC metastasis), for treatment of heparanase-associated diseases (e.g.
CC tumours, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
CC mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
CC metastases) derived from liver, prostate, bladder, breast, ovary,
CC cervix, colon, skin, intestine, stomach, uterus and pancreas, kidney
CC disease, diabetes and inflammation, haemorrhagic nephritis, nephrotic
CC syndrome, sepsis and inflammatory or autoimmune disease), for targeted
CC drug delivery (e.g. of anticancer agents) and as research reagents.
CC The present sequence represents a PCR primer for human heparanase, which
CC is used in an example from the present invention.
XX
SQ Sequence 24 BP; 7 A; 4 C; 6 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	439	Length:	24
Score:	53.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.86%	Indels:	0
DB:	21	Gaps:	0

US-09-899-440-18 (1-545) x AAZ33294 (1-24)

```
Qy    293 AspSerValThrTrpHisHisTyr 300
          ||||||||||||||||||||||
Db     24 GATTCAGTTACATGGCATCACTAC 1
```

RESULT 7
ABN86005
ID ABN86005 standard; DNA; 30 BP.
XX
AC ABN86005;
XX
DT 06-SEP-2002 (first entry)
XX
DE Human heparanase gene specific primer HP-6.
XX
KW Human; heparanase; cytostatic; vasotropic; antidiabetic; anti-HIV;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic;
KW antianaemic; neuroprotective; nootropic; cerebroprotective;
KW antibacterial; virucide; protozoacide; fungicide; antiinflammatory;
KW cardiant; immunosuppressive; tumour metastasis; inflammatory disease;
KW allograft rejection; cell migration; angiogenesis; basement membrane;
KW extracellular matrix; cancer; ischaemia; diabetic retinopathy;
KW macular degeneration; rheumatoid arthritis; psoriasis; HIV infection;
KW sickle cell anaemia; Alzheimer's disease; muscular dystrophy;
KW neurodegenerative disease; vascular disease; cardiovascular disease;
KW cystic fibrosis; stroke; gene therapy; PCR; primer; ss.
XX

OS Homo sapiens.
XX
PN WO200244353-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US44798.
XX
PR 30-NOV-2000; 2000US-250690P.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Wolffe AP, Qi H;
XX
DR WPI; 2002-527708/56.
XX
PT New heparanase polynucleotide, useful for controlling disease states
PT such as tumour metastasis, inflammatory diseases and allograft rejection
PT
XX
PS Example 1; Page 44; 72pp; English.
XX
CC The invention relates to novel heparanase sequences, particularly novel
CC sequences from the regulatory regions upstream and downstream of the
CC coding region. The activity of polynucleotides of the invention may be
CC described as, cytostatic, vasotropic, antidiabetic, anti-HIV,
CC ophthalmological, antirheumatic, antiarthritic, antipsoriatic,
CC antianaemic, neuroprotective, nootropic, cerebroprotective,
CC antibacterial, virucide, protozoacide, fungicide, antiinflammatory,
CC cardiant and immunosuppressive. Modulating expression of heparanase gene
CC using constructs of the invention is useful for facilitating targeted
CC control of disease states such as tumour metastasis, inflammatory
CC diseases, allograft rejection, and for inhibiting processes such as cell
CC migration, angiogenesis, and degradation of the basement membrane and/or
CC extracellular matrix. Heparanase-targeted DNA binding domains modulates
CC gene expression, and are useful for therapeutic or prophylactic
CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular
CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell
CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative
CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,
CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs
CC of the invention may also be useful in gene therapy. The current sequence
CC represents a human heparanase gene specific primer designated HP-6. This
CC was used in the determination of nucleotide sequences in the human
CC heparanase gene and flanking regions.
XX
SQ Sequence 30 BP; 4 A; 9 C; 9 G; 8 T; 0 other;

Alignment Scores:

Pred. No.:	2.68e+03	Length:	30
Score:	47.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.65%	Indels:	0
DB:	24	Gaps:	0

US-09-899-440-18 (1-545) x ABN86005 (1-30)

```
Qy      38 GlnAspValValAspLeuAspPhePhe 46
           |||||||||||||||||||||||||||
Db       4 CAGGACGTCGTGGACCTGGACTTCTTC 30
```

RESULT 8
AAZ11239
ID AAZ11239 standard; DNA; 40 BP.
XX
AC AAZ11239;
XX
DT 15-NOV-1999 (first entry)
XX
DE PCR primer for human pre-proheparanase coding sequence.
XX
KW Human; pre-proheparanase; platelet; wound healing; angiogenesis blocker;
KW inflammation; psoriasis; diabetic retinopathy; solid tumour; arthritis;
KW heparin degradation; anticoagulant neutralisation; asthma; CNS disease;
KW inflammatory disease; vascular restenosis; atherosclerosis; diagnosis;
KW tumour growth; fibroproliferative disorder; neurodegenerative disease;
KW therapy; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9943830-A2.
XX
PD 02-SEP-1999.
XX
PF 18-FEB-1999; 99WO-US01489.
XX
PR 26-MAR-1998; 98US-0079401.
PR 24-FEB-1998; 98US-0075706.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Fairbanks MB, Heinrikson RL, Mildner AM;
XX
DR WPI; 1999-540598/45.
XX
PT New isolated platelet heparanase polypeptides, used to develop
PT products for, e.g. wound healing and blocking angiogenesis
XX
PS Example 6; Page 24; 57pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the human
CC pre-proheparanase of the invention. The pre-proheparanase sequence was
CC isolated from human platelets. The heparanase can be used for identifying
CC agents which alter heparanase activity. The heparanase can be used for
CC wound healing or for blocking angiogenesis or inflammation. It can be
CC used for treating e.g. psoriasis, diabetic retinopathy or solid tumours,
CC or for the degradation of heparin and the neutralisation of heparin's
CC anticoagulant properties during surgery. Inhibitors of heparanase
CC activity can be used in the treatment of arthritis, asthma, and other
CC inflammatory diseases, vascular restenosis, atherosclerosis, tumour
CC growth and progression, fibroproliferative disorders, and central nervous
CC system (CNS) and neurodegenerative diseases. The products can also be
CC used for detection and diagnosis. The purified heparanase, both
CC recombinantly produced human heparanase and heparanase isolated from
CC human platelet activity, allows for the convenient selection of compounds
CC having anti-heparanase activity, i.e. inhibitors of heparanase activity,
CC by measuring inhibition of heparanase activity. Inhibition of heparanase
CC activity can be measured by blocking heparanase-mediated release of
CC radioactive fragments from in vivo radiolabelled (HSPG)/heparin.
XX
SQ Sequence 40 BP; 16 A; 10 C; 7 G; 7 T; 0 other;

Alignment Scores:

Pred. No.:	4.15e+03	Length:	40
Score:	47.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.65%	Indels:	0
DB:	20	Gaps:	0

US-09-899-440-18 (1-545) x AAZ11239 (1-40)

```
Qy     160 LysLysPheLysAsnSerThrTyrSer 168
           |||||||||||||||||||||||||||
Db      14 AAAAAGTTCAAGAACAGCACCTACTCA 40
```

RESULT 9
AAZ47781/c
ID AAZ47781 standard; DNA; 32 BP.
XX
AC AAZ47781;
XX
DT 02-MAR-2000 (first entry)
XX

DE Heparanase expression vector construction PCR primer SEQ ID NO:18.
XX
KW Human; heparanase; hpa; genetic modification; expression; anticancer;
KW angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumour;
KW anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
KW heparan sulphate; heparin-binding growth factor; tumour angiogenesis;
KW metastasis; wound healing; restenosis; atherosclerosis; inflammation;
KW neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
KW micrometastasis; autoimmune lesion; kidney failure; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9957244-A1.
XX
PD 11-NOV-1999.
XX
PF 29-APR-1999; 99WO-US09256.
XX
PR 01-MAY-1998; 98US-0071618.
PR 02-MAR-1999; 99US-0260038.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (FRIE/) FRIEDMAN M M.
XX
PI Ben-Artzi H, Ayal-Hershkovitz M, Yacoby-Zeevi O, Pecker I, Peleg Y;
PI Shlomi Y;
XX
DR WPI; 2000-062144/05.
XX
PT Engineered cells that express recombinant heparanase, useful
PT therapeutically, e.g. for treating angiogenesis and to screen for
PT specific inhibitors, potential anticancer agents -
XX
PS Example 6; Page 54; 118pp; English.
XX
CC The present invention describes genetically modified cells (A) containing
CC a polynucleotide (I) that encodes a polypeptide with heparanase activity,
CC and express recombinant heparanase (II). Heparanase cleaves heparan
CC sulphate (HS) at specific intrachain sites, resulting in release of
CC heparin-binding growth factors, enzymes and proteins that are sequestered
CC by HS in basement membranes, extracellular matrix or cell surfaces. It
CC may also be implicated in tumour angiogenesis and metastases. (II) is
CC potentially useful in wound healing and for treating angiogenesis,
CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral
CC infection and cystic fibrosis. It can also be used to neutralise heparin
CC (an alternative to protamine) and to screen for specific inhibitors
CC (potentially useful for treating cancer and metastases). Antibodies
CC raised against (II) are used for immunodetection and diagnosis of
CC micrometastases, autoimmune lesions and kidney failure. (A) provide (II)
CC in large quantities, in a form that is homogeneously processed and
CC activated/neutralised by a dedicated protease. The present sequence
CC represents a PCR primer used in the construction of a heparanase
CC expression vector in an example from the present invention.
XX
SQ Sequence 32 BP; 8 A; 11 C; 4 G; 9 T; 0 other;

Alignment Scores:

Pred. No.:	3.78e+03	Length:	32
Score:	46.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	1.61%	Indels:	0
DB:	21	Gaps:	0

US-09-899-440-18 (1-545) x AAZ47781 (1-32)

```
Qy    114 PheGluGluArgSerTyrTrpGlnSer 122
          ||||||||||||||||||||   |||
Db     31 TTTGAAGAGAGAAGTTACTGGGCATCG 5
```

RESULT 10
AAI67044

ID AAI67044 standard; DNA; 25 BP.
XX
AC AAI67044;
XX
DT 11-FEB-2002 (first entry)
XX
DE Human heparanase-like enzyme (HLE) antisense oligo 5.
XX
KW HLE; heparanase-like enzyme; cytostatic; vasotropic; antiatherosclerotic;
KW antiinflammatory; nootropic; neuroprotective; virucide; antibacterial;
KW protozoacide; vulnerary; gene therapy; antisense; human; ss.
XX
OS Homo sapiens.
XX
PN WO200172973-A2.
XX
PD 04-OCT-2001.
XX
PF 22-FEB-2001; 2001WO-EP01997.
XX
PR 24-FEB-2000; 2000US-184660P.
PR 27-NOV-2000; 2000US-252913P.
XX
PA (FARB) BAYER AG.
XX
PI Ramakrishnan S;
XX
DR WPI; 2001-639227/73.
XX
PT New human heparanase-like enzyme polypeptide and polynucleotide for
PT regulating extracellular matrix degradation and treating metastatic
PT cancer, atherosclerosis, neurodegenerative diseases and pathogenic
PT infections -
XX
PS Example 5; Page 60; 82pp; English.
XX
CC The invention provides polynucleotides encoding heparanase-like enzyme
CC (HLE) polypeptides. The HLE polypeptides can be expressed by standard
CC recombinant methodology. The HLE modulators are useful for regulating
CC extracellular matrix degradation, to suppress metastatic activity of
CC malignant cells, to enhance extracellular matrix degradation during
CC development and to regulate tumour angiogenesis. HLE is useful for
CC regulating degradation of the extracellular matrix for the treatment of
CC various diseases, to develop diagnostic assays for these diseases and
CC to provide new tools for basic research in medicine and biology. HLE is
CC useful for developing new drugs to inhibit tumour cell metastasis,
CC inflammation and autoimmunity, to modulate bioavailability of heparin-
CC binding growth factors, cellular responses to heparin-binding growth
CC factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoan, and bacterial infections and
CC disintegration of neurodegenerative plaques. HLE and regulators of HLE
CC are useful for treating wound healing, angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases such as
CC Creutzfeldt-Jakob diseases, Scrapie and Alzheimer's diseases and viral,
CC bacterial and protozoan infections. HLE can also be used to neutralize
CC plasma heparin, as a potential replacement of protamine. HLE is useful
CC for producing antibodies specific for the polypeptide, which can be
CC applied for immunodetection and diagnosis of micrometastases, autoimmune
CC lesions, and renal failure in biopsy specimens, plasma samples and body
CC fluids. The agents identified by the screening assays are useful in
CC animal models to determine the efficacy, toxicity or side effects of
CC treatment with the agent and to determine mechanism of action of the
CC agent. Antisense oligonucleotides are useful for modulating HLE gene
CC expression. The present sequence represents an antisense oligo specific
CC for the human HLE mRNA.
XX
SQ Sequence 25 BP; 4 A; 10 C; 3 G; 8 T; 0 other;

Alignment Scores:

Pred. No.:	5.42e+03	Length:	25
Score:	43.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	87.50%	Mismatches:	0

```
Query Match:            1.51%       Indels:        0
DB:                     22          Gaps:          0

US-09-899-440-18 (1-545) x AA167044 (1-25)

Qy    405 AspTyrTrpLeuSerLeuLeuPhe 412
          |||||||||||||||||||:::
Db      1 GACTACTGGCTCTCTCCTCTAC 24

RESULT 11
AAZ11243
ID   AAZ11243 standard; DNA; 35 BP.
XX
AC   AAZ11243;
XX
DT   15-NOV-1999  (first entry)
XX
DE   PCR primer for human pre-proheparanase coding sequence.
XX
KW   Human; pre-proheparanase; platelet; wound healing; angiogenesis blocker;
KW   inflammation; psoriasis; diabetic retinopathy; solid tumour; arthritis;
KW   heparin degradation; anticoagulant neutralisation; asthma; CNS disease;
KW   inflammatory disease; vascular restenosis; atherosclerosis; diagnosis;
KW   tumour growth; fibroproliferative disorder; neurodegenerative disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9943830-A2.
XX
PD   02-SEP-1999.
XX
PF   18-FEB-1999;   99WO-US01489.
XX
PR   26-MAR-1998;   98US-0079401.
PR   24-FEB-1998;   98US-0075706.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Fairbanks MB,  Heinrikson RL,  Mildner AM;
XX
DR   WPI; 1999-540598/45.
XX
PT   New isolated platelet heparanase polypeptides, used to develop
PT   products for, e.g. wound healing and blocking angiogenesis
XX
PS   Example 7; Page 27; 57pp; English.
XX
CC   This sequence represents a PCR primer for DNA encoding the human
CC   pre-proheparanase of the invention. The pre-proheparanase sequence was
CC   isolated from human platelets. The heparanase can be used for identifying
CC   agents which alter heparanase activity. The heparanase can be used for
CC   wound healing or for blocking angiogenesis or inflammation. It can be
CC   used for treating e.g. psoriasis, diabetic retinopathy or solid tumours,
CC   or for the degradation of heparin and the neutralisation of heparin's
CC   anticoagulant properties during surgery. Inhibitors of heparanase
CC   activity can be used in the treatment of arthritis, asthma, and other
CC   inflammatory diseases, vascular restenosis, atherosclerosis, tumour
CC   growth and progression, fibroproliferative disorders, and central nervous
CC   system (CNS) and neurodegenerative diseases. The products can also be
CC   used for detection and diagnosis. The purified heparanase, both
CC   recombinantly produced human heparanase and heparanase isolated from
CC   human platelet activity, allows for the convenient selection of compounds
CC   having anti-heparanase activity, i.e. inhibitors of heparanase activity,
CC   by measuring inhibition of heparanase activity. Inhibition of heparanase
CC   activity can be measured by blocking heparanase-mediated release of
CC   radioactive fragments from in vivo radiolabelled (HSPG)/heparin.
XX
SQ   Sequence 35 BP; 15 A; 8 C; 6 G; 6 T; 0 other;

Alignment Scores:
Pred. No.:              9.03e+03    Length:        35
Score:                  43.00       Matches:       8
Percent Similarity:     100.00%     Conservative:  0
Best Local Similarity:  100.00%     Mismatches:    0
Query Match:            1.51%       Indels:        0
DB:                     20          Gaps:          0

US-09-899-440-18 (1-545) x AAZ11243 (1-35)

Qy    160 LysLysPheLysAsnSerThrTyr 167
          |||||||||||||||||||||||
Db     12 AAAAAGTTCAAGAACAGCACCTAC 35

RESULT 12
AAQ55601/c
ID   AAQ55601 standard; DNA; 40 BP.
XX
AC   AAQ55601;
XX
DT   14-JUL-1994  (first entry)
XX
DE   Flanking sequences for manipulation of cloned insert.
XX
KW   Polymerase chain reaction; mutation; mutagenesis; alteration;
KW   deletion; insertion; repetition; amplification; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   primer_bind      1..20
FT                    /*tag=  a
FT   primer_bind      21..40
FT                    /*tag=  b
FT   misc_feature     20..21
FT                    /*tag=  c
FT                    /note= "insertion site for cloned DNA"
XX
PN   US5279952-A.
XX
PD   18-JAN-1994.
XX
PF   09-AUG-1991;   91US-0743245.
XX
PR   09-AUG-1991;   91US-0743245.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wu KC;
XX
DR   WPI; 1994-034337/04.
XX
PT   Construction of altered DNA molecules - using polymerase chain
PT   reaction to amplify a segment of a cloned segment of DNA obtd. by
PT   endonuclease cleavage
XX
PS   Disclosure; Column 17; 24pp; English.
XX
CC   This synthetic sequence is used to illustrate the novel method; a
CC   direct repeat of a specific cloned region of DNA which lies between
CC   the flanking sequences can be constructed using primers having the
CC   sequences in AAQ55602-Q55605.
XX
SQ   Sequence 40 BP; 14 A; 7 C; 13 G; 6 T; 0 other;

Alignment Scores:
Pred. No.:              1.11e+04    Length:        40
Score:                  43.00       Matches:       6
Percent Similarity:     84.62%      Conservative:  5
Best Local Similarity:  46.15%      Mismatches:    2
Query Match:            1.51%       Indels:        0
DB:                     15          Gaps:          0

US-09-899-440-18 (1-545) x AAQ55601 (1-40)
```

```
Qy       7 ProAlaLeuProProProLeuLeuMetLeuLeuLeuLeu 19
           |||       |||||||||||||:::|||:::::::::::::
Db      39 CCTCCTCCTCCTCCTCCTCTGATGATGATGATGATGATG 1

RESULT 13
AAH96175
ID   AAH96175 standard; RNA; 38 BP.
XX
AC   AAH96175;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human Chk1 ribozyme SEQ ID NO: 1600.
XX
KW   Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
KW   RNA cleavage; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157206-A2.
XX
PD   09-AUG-2001.
XX
PF   02-FEB-2001; 2001WO-US03504.
XX
PR   03-FEB-2000; 2000US-0179983.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (FATT/) FATTAEY A R.
XX
PI   Fattaey AR,  Jarvis T,  McSwiggen J,  Booher RN,  Holman PS;
XX
DR   WPI; 2001-496922/54.
XX
PT   Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT   molecules, which downregulates expression of a checkpoint kinase-1
PT   gene, useful for treating colorectal, lung, breast or prostate cancers
PT   -
XX
PS   Claim 5; Page 55; 115pp; English.
XX
CC   The present invention provides nucleic acid molecules capable of
CC   downregulating the expression of the human checkpoint kinase-1 (Chk1)
CC   gene. These may be antisense or ribozyme sequences, and are useful in the
CC   treatment of diseases associated with conditions affected by Chk1 levels,
CC   including cancer. The present sequence is an oligonucleotide described in
CC   the exemplification of the invention.
XX
SQ   Sequence 38 BP; 9 A; 7 C; 14 G; 8 U; 0 other;

Alignment Scores:
Pred. No.:                1.31e+04        Length:          38
Score:                    42.00           Matches:         8
Percent Similarity:       81.82%          Conservative:    1
Best Local Similarity:    72.73%          Mismatches:      2
Query Match:              1.47%           Indels:          0
DB:                       22              Gaps:            0

US-09-899-440-18 (1-545) x AAH96175 (1-38)

Qy     480 TyrLeuLeuArgProLeuGlyProHisGlyLeu 490
           ||||||:::|||||||||||||||      ||||||
Db       6 UAUCUGAUGAGGCCGUUAGGCCGAAAGGGGCUG 38

RESULT 14
AAF81504/c
ID   AAF81504 standard; DNA; 40 BP.
XX
AC   AAF81504;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Novel human G protein coupled receptor coding sequence PCR primer #1.
XX
KW   Human; G protein coupled receptor; central nervous system disease;
KW   schizophrenia; Parkinson's disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001029083-A.
XX
PD   06-FEB-2001.
XX
PF   23-JUL-1999;   99JP-0209918.
XX
PR   23-JUL-1999;   99JP-0209918.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
DR   WPI; 2001-221498/23.
XX
PT   A new G protein coupled receptor  -
XX
PS   Example 2; Page 12; 14pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences for a
CC   novel human G protein coupled receptor. This is useful in the
CC   identification of treatments for central nervous system diseases such as
CC   schizophrenia, Parkinson's disease and aches.
XX
SQ   Sequence 40 BP; 10 A; 8 C; 4 G; 18 T; 0 other;

Alignment Scores:
Pred. No.:                1.41e+04        Length:          40
Score:                    42.00           Matches:         7
Percent Similarity:       92.31%          Conservative:    5
Best Local Similarity:    53.85%          Mismatches:      1
Query Match:              1.47%           Indels:          0
DB:                       22              Gaps:            0

US-09-899-440-18 (1-545) x AAF81504 (1-40)

Qy      72 ArgPheLeuIleLeuLeuGlySerProLysLeuArgThr 84
           :::::::::|||||||:::   ||||||||||:::|||||||
Db      40 AAGTATATGATTCTTATAGAAAGTCCAAAAGTAAGGACA 2

RESULT 15
AAF87604/c
ID   AAF87604 standard; DNA; 40 BP.
XX
AC   AAF87604;
XX
DT   11-JUL-2001  (first entry)
XX
DE   DNA associated with human G protein coupling receptor.
XX
KW   Human; G protein coupling receptor; CNS; central nervous system; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001054389-A.
XX
PD   27-FEB-2001.
XX
PF   17-AUG-1999;   99JP-0230777.
XX
PR   17-AUG-1999;   99JP-0230777.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
DR   WPI; 2001-321039/34.
XX
PT   A novel G protein coupling receptor.  -
XX
PS   Disclosure; Page 12; 14pp; Japanese.
XX
```

CC The present invention relates to a novel G protein coupling
CC receptor, a gene encoding for the receptor family, a process for
CC preparation of the receptor family, an antibody to the receptor
CC family and a method for screening using the receptor. The invention may
CC be used for screening of agents expected to be useful for
CC prevention and treatment of central nervous system (CNS) diseases.
CC The present sequence is DNA associated with the G protein
CC coupling receptor.
XX
SQ Sequence 40 BP; 10 A; 8 C; 4 G; 18 T; 0 other;

Alignment Scores:

Pred. No.:	1.41e+04	Length:	40
Score:	42.00	Matches:	7
Percent Similarity:	92.31%	Conservative:	5
Best Local Similarity:	53.85%	Mismatches:	1
Query Match:	1.47%	Indels:	0
DB:	22	Gaps:	0

US-09-899-440-18 (1-545) x AAF87604 (1-40)

```
Qy      72 ArgPheLeuIleLeuLeuGlySerProLysLeuArgThr 84
           :::::::::||||||:::  ||||||||||:::||||||
Db      40 AAGTATATGATTCTTATAGAAAGTCCAAAAGTAAGGACA 2
```

Search completed: January 10, 2003, 12:30:32
Job time : 313 secs

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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2003, 12:23:22 ; Search time 2175 Seconds
(without alignments)
4058.179 Million cell updates/sec

Title: US-09-899-440-18
Perfect score: 2850
Sequence: 1 MLLRSKPALPPPLLMLLLLG.....LPAFSYSFFVIRNAKVAACI 545

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 60474

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09899440/runat_08012003_124403_23170/app_query.fasta_1.711
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=40
-USER=US09899440_@CGN_1_1_1439_@runat_08012003_124403_23170 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	41.5	1.5	40	17	AZ345503	AZ345503 1M0080G05
	2	41	1.4	36	13	BI819025	BI819025 603033150
c	3	40	1.4	36	17	AZ328880	AZ328880 1M0052D19
c	4	40	1.4	37	13	BI765481	BI765481 603050546
c	5	39	1.4	37	17	AZ761912	AZ761912 1M0556D02
	6	38	1.3	26	17	BH810301	BH810301 SALK_0488
	7	38	1.3	31	9	AA932800	AA932800 oo60f10.s
	8	38	1.3	40	9	AI800161	AI800161 tr23b08.x
	9	37	1.3	31	9	AI633407	AI633407 to46d08.x
c	10	37	1.3	38	17	AZ783438	AZ783438 2M0025H12
c	11	37	1.3	40	9	AA878864	AA878864 of84g05.s
	12	37	1.3	40	17	BH626944	BH626944 1007066F1
c	13	36	1.3	25	17	AZ635993	AZ635993 1M0493E20
c	14	36	1.3	30	17	AZ786025	AZ786025 2M0030O16
c	15	36	1.3	31	9	AA779867	AA779867 af46a11.s
c	16	36	1.3	33	10	AV947529	AV947529 AV947529
c	17	36	1.3	33	17	AZ607132	AZ607132 1M0429J23
c	18	36	1.3	34	12	BE914450	BE914450 601668834
c	19	36	1.3	34	17	AZ304044	AZ304044 1M0003O20
	20	36	1.3	36	17	TA207D04Q	AL475845 T. brucei
c	21	36	1.3	37	9	AI624760	AI624760 ts44b02.x
	22	36	1.3	37	17	AZ773664	AZ773664 2M0001H14
c	23	36	1.3	38	10	AW248989	AW248989 2820892.5
c	24	36	1.3	40	9	AI288030	AI288030 qu99e04.x
	25	36	1.3	40	9	AI783759	AI783759 tu45d08.x
c	26	36	1.3	40	17	AZ957172	AZ957172 2M0223O23
c	27	35	1.2	25	17	AZ608629	AZ608629 1M0433A05
c	28	35	1.2	30	12	BE904656	BE904656 601498767
	29	35	1.2	31	9	AI364457	AI364457 qw38e11.x
	30	35	1.2	31	12	BF666846	BF666846 602121169
c	31	35	1.2	33	13	BI829936	BI829936 603080061
c	32	35	1.2	34	9	AI679919	AI679919 tu67d10.x
c	33	35	1.2	34	9	AI793680	AI793680 fc50d11.x
	34	35	1.2	34	17	AZ825014	AZ825014 2M0100A06
c	35	35	1.2	35	17	TA363G02P	AL494295 T. brucei
	36	35	1.2	36	17	BH857106	BH857106 SALK_0768
c	37	35	1.2	37	9	AI913033	AI913033 tz75d02.x
c	38	35	1.2	37	9	AU257109	AU257109 AU257109
c	39	35	1.2	37	17	AZ625706	AZ625706 1M0465O23
	40	35	1.2	38	17	AZ662464	AZ662464 1M0541O03
	41	35	1.2	39	17	AZ946046	AZ946046 2M0207I08
	42	35	1.2	39	17	BH792015	BH792015 SALK_0623
c	43	35	1.2	40	9	AI628006	AI628006 ty21d06.x
	44	35	1.2	40	9	AI678633	AI678633 tu84h12.x
c	45	35	1.2	40	14	D18217	D18217 MUSGS00491

ALIGNMENTS

RESULT 1
AZ345503
LOCUS AZ345503 40 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080G05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G05 F, DNA sequence.
ACCESSION AZ345503
VERSION AZ345503.1 GI:10424740
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 40.

FEATURES Location/Qualifiers
source 1. .40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 24 c 0 g 15 t
ORIGIN

Alignment Scores:

Pred. No.:	5.6e+04	Length:	40
Score:	41.50	Matches:	10
Percent Similarity:	92.31%	Conservative:	2
Best Local Similarity:	76.92%	Mismatches:	0
Query Match:	1.46%	Indels:	1
DB:	17	Gaps:	1

US-09-899-440-18 (1-545) x AZ345503 (1-40)

```
Qy       8 AlaLeuPro---ProProLeuLeuMetLeuLeuLeuLeu 19
           :::||||||   ||||||||||||:::|||||||||||||
Db       1 TCCCTCCCCCTCCCTCCTCTCCTTCTCCTTCTACTCCTT 39
```

RESULT 2
BI819025
LOCUS BI819025 36 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033150F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174340 5', mRNA sequence.
ACCESSION BI819025
VERSION BI819025.1 GI:15930575
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11434 row: c column: 13
High quality sequence stop: 36.

FEATURES Location/Qualifiers
source 1. .36
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5174340"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 7 a 20 c 6 g 3 t
ORIGIN

Alignment Scores:

Pred. No.:	5.4e+04	Length:	36
Score:	41.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	5
Best Local Similarity:	50.00%	Mismatches:	0
Query Match:	1.44%	Indels:	0
DB:	13	Gaps:	0

US-09-899-440-18 (1-545) x BI819025 (1-36)

```
Qy     469 ProTyrProPheSerAsnLysGlnValAsp 478
           |||||||||:::::::|||:::::::::|||
Db       4 CCATACCCCTACGCCAACCGCCGCCTGGAC 33
```

RESULT 3
AZ328880/c
LOCUS AZ328880 36 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0052D19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0052D19 R, DNA sequence.
ACCESSION AZ328880
VERSION AZ328880.1 GI:10389043
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 36)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: D column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.

FEATURES Location/Qualifiers
source 1. .36
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0052D19"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 3 c 15 g 10 t
ORIGIN

Alignment Scores:

Pred. No.:	7.14e+04	Length:	36
Score:	40.00	Matches:	7
Percent Similarity:	81.82%	Conservative:	2
Best Local Similarity:	63.64%	Mismatches:	2
Query Match:	1.40%	Indels:	0
DB:	17	Gaps:	0

US-09-899-440-18 (1-545) x AZ328880 (1-36)

```
Qy      6 LysProAlaLeuProProProLeuLeuMetLeu 16
          ||||||:::  ||||||||||||:::  |||
Db     36 AAGCCAAGTCCACCACCTCCTCTTATCAGCTTA 4
```

RESULT 4
BI765481/c
LOCUS BI765481 37 bp mRNA linear EST 25-SEP-2001
DEFINITION 603050546F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190683 5', mRNA sequence.
ACCESSION BI765481
VERSION BI765481.1 GI:15757059
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11476 row: 1 column: 12
High quality sequence stop: 37.

FEATURES Location/Qualifiers
source 1. .37
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5190683"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 7 a 6 c 22 g 2 t
ORIGIN

Alignment Scores:

Pred. No.:	7.48e+04	Length:	37
Score:	40.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.40%	Indels:	0
DB:	13	Gaps:	0

US-09-899-440-18 (1-545) x BI765481 (1-37)

```
Qy     27 ProGlyAlaLeuProArgPro 33
          |||||||||||||||||||||
Db     37 CCGGGGGCTCTCCCTCGCCCA 17
```

RESULT 5
AZ761912/c
LOCUS AZ761912 37 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0556D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0556D02 R, DNA sequence.
ACCESSION AZ761912
VERSION AZ761912.1 GI:12871332
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 37)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0556 row: D column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.

```
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0556D02"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       14 a      1 c     22 g      0 t
ORIGIN
```

Alignment Scores:

Pred. No.:	9.9e+04	Length:	37
Score:	39.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	1.37%	Indels:	0
DB:	17	Gaps:	0

US-09-899-440-18 (1-545) x AZ761912 (1-37)

```
Qy       7 ProAlaLeuProProProLeuLeu 14
           |||   ||||||||||||||||||
Db      31 CCTCCTCTTCCTCCTCCTCTTCTG 8
```

RESULT 6
BH810301

```
LOCUS       BH810301                  26 bp    DNA     linear   GSS 02-MAY-2002
DEFINITION  SALK_048826 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_048826, DNA sequence.
ACCESSION   BH810301
VERSION     BH810301.1  GI:20388119
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_048826"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       10 a      1 c      7 g      8 t
ORIGIN
```

Alignment Scores:

Pred. No.:	7.23e+04	Length:	26
Score:	38.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	1.33%	Indels:	0
DB:	17	Gaps:	0

US-09-899-440-18 (1-545) x BH810301 (1-26)

```
Qy     217 GlyTyrAsnIleSerTrpGlu 223
           ||||||||||||   ||||||
Db       5 GGATATAATATATGTTGGGAA 25
```

RESULT 7
AA932800

```
LOCUS       AA932800                  31 bp    mRNA    linear   EST 07-JUL-1998
DEFINITION  oo60f10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570603 3'
            similar to TR:Q24423 Q24423 ZINC FINGER PROTEIN. ;, mRNA sequence.
ACCESSION   AA932800
VERSION     AA932800.1  GI:3086765
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 531  Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 3.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1570603"
                     /clone_lib="NCI_CGAP_Lu5"
```

/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 7 a 16 c 5 g 3 t
ORIGIN

Alignment Scores:

Pred. No.:	9.72e+04	Length:	31
Score:	38.00	Matches:	6
Percent Similarity:	90.00%	Conservative:	3
Best Local Similarity:	60.00%	Mismatches:	1
Query Match:	1.33%	Indels:	0
DB:	9	Gaps:	0

US-09-899-440-18 (1-545) x AA932800 (1-31)

```
Qy     508 GlnThrLeuProProLeuMetGluLysPro 517
           |||   |||||||||||:::::::::|||
Db       1 CAGCCGCTACCACCCCTACTCCAAGAGCCC 30
```

RESULT 8
AI800161
LOCUS AI800161 40 bp mRNA linear EST 06-JUL-1999
DEFINITION tr23b08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219127 3' similar to SW:CA13_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN. ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION AI800161
VERSION AI800161.1 GI:5365633
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2219127"
/clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

BASE COUNT 1 a 23 c 14 g 1 t 1 others
ORIGIN

Alignment Scores:

Pred. No.:	1.49e+05	Length:	40
Score:	38.00	Matches:	9
Percent Similarity:	52.94%	Conservative:	0
Best Local Similarity:	52.94%	Mismatches:	2
Query Match:	1.33%	Indels:	6
DB:	9	Gaps:	1

US-09-899-440-18 (1-545) x AI800161 (1-40)

```
Qy       8 AlaLeuProProProLeuLeuMetLeuLeuLeuLeuGlyProLeuGlyPro 24
           ||||||||||||||||                  ||||||   ||||||
Db       3 GCCCTCCCCCCCCCC----------------CCGGGCCCCGCGGGACCC 35
```

RESULT 9
AI633407
LOCUS AI633407 31 bp mRNA linear EST 14-DEC-1999
DEFINITION to46d08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2182095 3' similar to SW:PRP4_HUMAN P10163 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR ;contains TAR1.b2 MSR1 repetitive element ;, mRNA sequence.
ACCESSION AI633407
VERSION AI633407.1 GI:4684737
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1631 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2182095"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

BASE COUNT 5 a 17 c 5 g 4 t
ORIGIN

Alignment Scores:

Pred. No.:	1.29e+05	Length:	31
Score:	37.00	Matches:	6
Percent Similarity:	87.50%	Conservative:	1
Best Local Similarity:	75.00%	Mismatches:	1
Query Match:	1.30%	Indels:	0

```
DB:                 9          Gaps:          0

US-09-899-440-18 (1-545) x AI633407 (1-31)

Qy      5 SerLysProAlaLeuProProPro 12
          :::|||||||   ||||||||||||
Db      5 GCAAAACCCCTTTTACCCCCCCCC 28

RESULT 10
AZ783438/c
LOCUS       AZ783438                38 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0025H12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0025H12 F, DNA sequence.
ACCESSION   AZ783438
VERSION     AZ783438.1  GI:12918166
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0025  row: H  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0025H12"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       10 a      10 c      11 g       7 t
ORIGIN

Alignment Scores:

Pred. No.:                1.81e+05        Length:          38
Score:                    37.00           Matches:         7
Percent Similarity:       88.89%          Conservative:    1
Best Local Similarity:    77.78%          Mismatches:      1
Query Match:              1.30%           Indels:          0
DB:                       17              Gaps:            0

US-09-899-440-18 (1-545) x AZ783438 (1-38)

Qy     19 LeuGlyProLeuGlyProLeuSerPro 27
          ||||||||||:::|||   |||||||||
Db     33 CTTGGGCCCATGGGTATTCTCTCACCT 7

RESULT 11
AA878864/c
LOCUS       AA878864                40 bp    mRNA    linear   EST 25-MAR-1998
DEFINITION  of84g05.s1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1437080 3'
            similar to TR:Q15220 Q15220 PRPL-2 PROTEIN ;contains MER22.t2 MSR1
            repetitive element ;, mRNA sequence.
ACCESSION   AA878864
VERSION     AA878864.1  GI:2987829
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            unknown library type
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1437080"
                     /clone_lib="NCI_CGAP_Li5"
                     /tissue_type="hepatic adenoma"
                     /lab_host="DH10B"
                     /note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 0.8 kb."
BASE COUNT        4 a      13 c      20 g       3 t
ORIGIN

Alignment Scores:
Pred. No.:                1.98e+05        Length:          40
Score:                    37.00           Matches:         8
Percent Similarity:       76.92%          Conservative:    2
Best Local Similarity:    61.54%          Mismatches:      1
Query Match:              1.30%           Indels:          2
DB:                       9               Gaps:            1

US-09-899-440-18 (1-545) x AA878864 (1-40)

Qy     21 ProLeuGlyProLeuSerProGlyAlaLeuProArgPro 33
          |||:::|||      :::||||||||||   |||||||||
Db     39 CCGGTCGGG------AATCCCGGGGCGCCCCCCCGCCCC 7

RESULT 12
BH626944
LOCUS       BH626944                40 bp    DNA     linear   GSS 30-JAN-2002
DEFINITION  1007066F12.1EL_y1 1007 - RescueMu Grid H Zea mays genomic, DNA
            sequence.
ACCESSION   BH626944
VERSION     BH626944.1  GI:18440195
KEYWORDS    GSS.
SOURCE      Zea mays.
```

```
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1007066  column: 35
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Zea mays"
                     /cultivar="mixed background W23/A188/B73"
                     /db_xref="taxon:4577"
                     /clone_lib="1007 - RescueMu Grid H"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units.  For more information on RescueMu, go to the  web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.'  Grid H was grown at Berkeley in 2001.  DNA
                     was extracted from leaf punches,  double digested using
                     BamHI and BglII, and ligated to form circular plasmids.
                     DH10B cells were transformed and then screened on LB
                     plates with ampicillin."
BASE COUNT        7 a     12 c     10 g     11 t
ORIGIN

Alignment Scores:
Pred. No.:                1.98e+05        Length:          40
Score:                    37.00           Matches:         7
Percent Similarity:       81.82%          Conservative:    2
Best Local Similarity:    63.64%          Mismatches:      2
Query Match:              1.30%           Indels:          0
DB:                       17              Gaps:            0

US-09-899-440-18 (1-545) x BH626944 (1-40)

Qy       4 ArgSerLysProAlaLeuProProProLeuLeu 14
           ||||||   |||||||::   |||||||:::|||
Db       3 AGATCCGCCCCTGCTGTTGTACCACCAGTGTTG 35

RESULT 13
AZ635993/c
LOCUS       AZ635993                 25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0493E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0493E20 R, DNA sequence.
ACCESSION   AZ635993
VERSION     AZ635993.1  GI:11758183
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0493  row: E  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0493E20"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       11 a      0 c     14 g      0 t
ORIGIN

Alignment Scores:
Pred. No.:                1.19e+05        Length:          25
Score:                    36.00           Matches:         7
Percent Similarity:       87.50%          Conservative:    0
Best Local Similarity:    87.50%          Mismatches:      1
Query Match:              1.26%           Indels:          0
DB:                       17              Gaps:            0

US-09-899-440-18 (1-545) x AZ635993 (1-25)

Qy      10 ProProProLeuLeuMetLeuLeu 17
             ||||||||||||||   ||||||
Db      24 CCTCCTCCTCTCCTCTCTCTTCTC 1

RESULT 14
AZ786025/c
LOCUS       AZ786025                 30 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0030016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0030016 R, DNA sequence.
ACCESSION   AZ786025
VERSION     AZ786025.1  GI:12923372
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0030  row: O  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0030016"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        9 a      12 c       5 g       4 t
ORIGIN

Alignment Scores:
Pred. No.:                1.61e+05        Length:          30
Score:                    36.00           Matches:         6
Percent Similarity:       85.71%          Conservative:    0
Best Local Similarity:    85.71%          Mismatches:      1
Query Match:              1.26%           Indels:          0
DB:                       17              Gaps:            0

US-09-899-440-18 (1-545) x AZ786025 (1-30)

Qy     336 ArgProGlyLysLysValTrp 342
           ||||||||||||   ||||||
Db      25 AGGCCTGGCAAGGTTGTTTGG 5

RESULT 15
AA779867/c
LOCUS       AA779867                 31 bp    mRNA    linear   EST 05-FEB-1998
DEFINITION  af46a11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
            IMAGE:1034684 3' similar to TR:O01900 O01900 CODED FOR BY C.
            ELEGANS CDNA YK144H11.5. ;, mRNA sequence.
ACCESSION   AA779867
VERSION     AA779867.1  GI:2839198
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1034684"
                     /clone_lib="Soares_total_fetus_Nb2HF8_9w"
                     /dev_stage="8-9 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from pooled 8-9 week
                     (total) fetus material with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCTTAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        6 a      13 c       12 g      0 t
ORIGIN

Alignment Scores:
Pred. No.:                1.7e+05         Length:          31
Score:                    36.00           Matches:         6
Percent Similarity:       100.00%         Conservative:    2
Best Local Similarity:    75.00%          Mismatches:      0
Query Match:              1.26%           Indels:          0
DB:                       9               Gaps:            0

US-09-899-440-18 (1-545) x AA779867 (1-31)

Qy     349 AlaTyrGlyGlyGlyAlaProLeu 356
           :::::|||||||||||||||||||
Db      28 TCTTGGGGGGGGGGGGCCCCCCTC 5


Search completed: January 10, 2003, 14:18:26
Job time : 2180 secs
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